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OM protein - protein search, using sw model

Run on: May 9, 2003, 16:16:25 ; Search time 35 Seconds
(without alignments)
807.118 Million cell updates/sec

Title: US-09-905-666a-55
Perfect score: 1088
Sequence: 1 MKEVRRRIIALVTILVSVT.....NSQVNSLKEGLNGGQNTN 212

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A_Geneseq_101002.*
2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT.*
5: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT.*
6: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT.*
7: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT.*
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19: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT.*
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22: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT.*
24: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1088	100.0	212	23	AAU83841
2	1067	98.1	212	23	AAU83847
3	1063	97.7	212	23	AAU83848
4	1061	97.5	212	23	AAU83844
5	1060	97.4	212	23	AAU83845
6	1047	96.2	212	23	AAU83846
7	1008	92.6	212	23	AAU83849
8	1007	92.6	212	23	AAU83842
9	1006	92.5	212	23	AAU83843
10	1006	92.5	212	23	AAU83855

11	992	91.2	212	23	AAU83856
12	989	90.9	212	23	AAU83854
13	925	85.0	180	23	AAU83894
14	921	84.7	180	23	AAU83890
15	918	84.4	180	23	AAU83884
16	917	84.3	180	23	AAU83885
17	917	84.3	180	23	AAU83893
18	914	84.0	180	23	AAU83864
19	913	83.9	180	23	AAU83886
20	911	83.7	212	23	AAU83857
21	909	83.5	180	23	AAU83861
22	909	83.5	180	23	AAU83883
23	909	83.5	212	23	AAU83858
24	908	83.5	180	23	AAU83888
25	907	83.4	180	23	AAU83870
26	907	83.4	180	23	AAU83889
27	907	83.4	180	23	AAU83891
28	906	83.3	180	23	AAU83868
29	906	83.3	180	23	AAU83869
30	906	83.3	180	23	AAU83892
31	904	83.1	180	23	AAU83862
32	904	83.1	212	23	AAU83850
33	903	83.0	180	23	AAU83880
34	902	82.9	180	23	AAU83873
35	901	82.8	180	23	AAU83863
36	901	82.8	180	23	AAU83867
37	898	82.5	180	23	AAU83866
38	897	82.4	180	23	AAU83871
39	895	82.3	180	23	AAU83872
40	893	82.1	180	23	AAU83874
41	892	82.0	180	23	AAU83887
42	891	81.9	180	23	AAU83882
43	887	81.5	180	23	AAU83875
44	887	81.5	180	23	AAU83881
45	883	81.2	180	23	AAU83876

ALIGNMENTS

RESULT 1
AAU83841
ID AAU83841 standard; Protein; 212 AA.
XX
AC AAU83841;
XX
DT 08-MAY-2002 (first entry)
XX
DE Bacillus lipase polypeptide #1.
XX
Lipase; Bacillus; animal feed; flavour modification; fat modification;
human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
gastrointestinal lipid related condition; antiinflammatory; respiratory;
gastrointestinal.
XX
OS Bacillus pumilus.
XX
PN WO200206457-A2.
XX
PD 24-JAN-2002.
XX
PF 13-JUL-2001; 2001WO-US22160.
XX
PR 13-JUL-2000; 2000US-217954P.
XX
PR 21-JUN-2001; 2001US-300378P.
XX
XX (MAXY-) MAXYGEN INC.
XX
XX Giver LJ, Minshall J, Vogel K;
XX
XX WPI; 2002-171805/22.
XX
XX

DR N-PSDB; ABR33819.
XX Nucleic acids encoding lipase enzymes which are useful as supplements
PT in animal feeds, as agents of flavour modification and for treating
PT Crohn's disease and coeliac disease -
XX
PS Claim 20; Page 138; 196pp; English.
XX
CC The invention relates to new Bacillus lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AA083841-AA083897 represent Bacillus lipase
CC polypeptides of the invention.
XX
SQ Sequence 212 AA;
Query Match 100.0%; Score 1088; DB 23; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.6e-103;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKFVKRRILAVTLVSVTSFLFAMOPSAKAEHNPPVVMHVGIGASYNFAGIKSYLSVQ 60
DB 1 MKFVKRRILAVTLVSVTSFLFAMOPSAKAEHNPPVVMHVGIGASYNFAGIKSYLSVQ 60
QY 61 GWSRGKLYAVDFMDKGTGNTNNGPVLSEFVOKVLDFTGAKKVDIVAHSMGANTPYIYIKN 120
DB 61 GWSRGKLYAVDFMDKGTGNTNNGPVLSEFVOKVLDFTGAKKVDIVAHSMGANTPYIYIKN 120
QY 121 LDGNGKIKENVTLLGAGNRSTSKALPGTDPNOKILYTSYSSADMIYWNYSKIDGAKNA 180
DB 121 LDGNGKIKENVTLLGAGNRSTSKALPGTDPNOKILYTSYSSADMIYWNYSKIDGAKNA 180
QY 181 QIHGVGHIGLLMSQVNSLKEGLNGGGQNTN 212
DB 181 QIHGVGHIGLLMSQVNSLKEGLNGGGQNTN 212
RESULT 2
AA083847 standard; Protein: 212 AA.
AC AA083847;
XX
DT 08-MAY-2002 (first entry)
XX
DE Bacillus lipase polypeptide #7.
XX
KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
KW gastrointestinal.
XX
OS Bacillus firmus.
XX
PN WO200206457-A2.
XX
PD 24-JAN-2002.
XX
PF 13-JUL-2001; 2001WO-US22160.
XX
PR 13-JUL-2000; 2000US-217954P.
XX
PR 21-JUN-2001; 2001US-300378P.
XX

PA (MAXY-) MAXYGEN INC.
XX
PI Glycer LJ, Minshull J, Vogel K;
XX
DR WPI: 2002-171805/22.
XX
DR N-PSDB; ABR33825.
XX
PT Nucleic acids encoding lipase enzymes which are useful as supplements
PT in animal feeds, as agents of flavour modification and for treating
PT Crohn's disease and coeliac disease -
XX
PS Claim 20; Page 139; 196pp; English.
XX
CC The invention relates to new Bacillus lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AA083841-AA083897 represent Bacillus lipase
CC polypeptides of the invention.
XX
SQ Sequence 212 AA;
Query Match 98.1%; Score 1067; DB 23; Length 212;
Best Local Similarity 98.6%; Pred. No. 2.3e-101;
Matches 209; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MKFVKRRILAVTLVSVTSFLFAMOPSAKAEHNPPVVMHVGIGASYNFAGIKSYLSVQ 60
DB 1 MKFVKRRILAVTLVSVTSFLFAMOPSAKAEHNPPVVMHVGIGASYNFAGIKSYLSVQ 60
QY 61 GWSRGKLYAVDFMDKGTGNTNNGPVLSEFVOKVLDFTGAKKVDIVAHSMGANTPYIYIKN 120
DB 61 GWSRGKLYAVDFMDKGTGNTNNGPVLSEFVOKVLDFTGAKKVDIVAHSMGANTPYIYIKN 120
QY 121 LDGNGKIKENVTLLGAGNRSTSKALPGTDPNOKILYTSYSSADMIYWNYSKIDGAKNA 180
DB 121 LDGNGKIKENVTLLGAGNRSTSKALPGTDPNOKILYTSYSSADMIYWNYSKIDGAKNA 180
QY 181 QIHGVGHIGLLMSQVNSLKEGLNGGGQNTN 212
DB 181 QIHGVGHIGLLMSQVNSLKEGLNGGGQNTN 212
RESULT 3
AA083848 standard; Protein: 212 AA.
AC AA083848;
XX
DT 08-MAY-2002 (first entry)
XX
DE Bacillus lipase polypeptide #8.
XX
KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
KW gastrointestinal.
XX
OS Bacillus badius.
XX
PN WO200206457-A2.
XX
PD 24-JAN-2002.
XX

PF 13-JUL-2001; 2001WO-US22160.
 XX
 XX 13-JUL-2000; 2000US-217954P.
 PR 21-JUN-2001; 2001US-300378P.
 XX
 PA (MAXY-) MAXYGEN INC.
 XX
 PI Giver LJ, Minshull J, Vogel K;
 XX
 XX WPI: 2002-171805/22.
 DR N-PSDB; ABK33826.
 XX
 PT Nucleic acids encoding lipase enzymes which are useful as supplements
 PT in animal feeds, as agents of flavour modification and for treating
 PT Crohn's disease and coeliac disease -
 XX
 PS Claim 20; Page 139; 196pp; English.
 XX
 CC The invention relates to new Bacillus lipase enzymes and the nucleic
 CC acids encoding them. The lipase polypeptides are useful as supplements in
 CC animal feeds, as agents of flavour modification and fat modification in
 CC human foodstuffs (e.g. cheese), as agents in the creation of food
 CC emulsifiers, as agents for tanning/processing of leather and as cleaning
 CC agents. They are also useful for treating Crohn's disease, cystic
 CC fibrosis, coeliac disease, indigestion, obesity and other
 CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
 CC conditions can be therapeutically or prophylactically treated via a
 CC method of hydrolysing a lipid comprising expressing in a target cell or
 CC contacting a target cell with an effective amount of DNA or protein of
 CC the invention. Sequences AA083841-AA083897 represent Bacillus lipase
 CC polypeptides of the invention.
 XX
 SQ Sequence 212 AA;
 Query Match 97.7%; Score 1063; DB 23; Length 212;
 Best Local Similarity 98.1%; Pred. No. 5.8e-101;
 Matches 208; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MKFVKRRRIALVTIILSVTSLFAMOPSAKAAEHNPVNVVHIGASYNFAGIKSYLSQ 60
 DB 1 MKFVKRRRIALVTIILSVTSLFAMOPSAKAAEHNPVNVVHIGASYNFAGIKSYLSQ 60
 QY 61 GMSRGLYAVDFWMDKTGTNYNNGPVLSPFYQVLDGTGAKKVDYAHSMGANTPYRYKN 120
 DB 61 GMSRGLYAVDFWMDKTGTNYNNGPVLSPFYQVLDGTGAKKVDYAHSMGANTPYRYKN 120
 QY 121 LDGKNKIEENVVTLGGANRSTSKALPGTDPNOKIILYTSYSSADMTVMYLSKLDGAKNV 180
 DB 121 LDGKNKIEENVVTLGGANRSTSKALPGTDPNOKIILYTSYSSADMTVMYLSKLDGAKNV 180
 QY 181 QIHGVGHIGLNMNSQVNSLIKEGLNGGONTN 212
 DB 181 QIHGVGHIGLNMNSQVNSLIKEGLNGGONTN 212
 RESULT 4
 AA083844
 ID AA083844 standard; Protein; 212 AA.
 XX
 AC AA083844;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Bacillus lipase polypeptide #4.
 XX
 KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
 KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
 KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
 KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
 KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
 KW gastrointestinal.
 XX
 OS Bacillus lentus.

XX
 PN WO200206457-A2.
 XX
 XX 24-JAN-2002.
 PD
 XX
 PF 13-JUL-2001; 2001WO-US22160.
 XX
 XX 13-JUL-2000; 2000US-217954P.
 PR 21-JUN-2001; 2001US-300378P.
 XX
 PA (MAXY-) MAXYGEN INC.
 XX
 PI Giver LJ, Minshull J, Vogel K;
 XX
 XX WPI: 2002-171805/22.
 DR N-PSDB; ABK33822.
 XX
 PT Nucleic acids encoding lipase enzymes which are useful as supplements
 PT in animal feeds, as agents of flavour modification and for treating
 PT Crohn's disease and coeliac disease -
 XX
 PS Claim 20; Page 138-139; 196pp; English.
 XX
 CC The invention relates to new Bacillus lipase enzymes and the nucleic
 CC acids encoding them. The lipase polypeptides are useful as supplements in
 CC animal feeds, as agents of flavour modification and fat modification in
 CC human foodstuffs (e.g. cheese), as agents in the creation of food
 CC emulsifiers, as agents for tanning/processing of leather and as cleaning
 CC agents. They are also useful for treating Crohn's disease, cystic
 CC fibrosis, coeliac disease, indigestion, obesity and other
 CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
 CC conditions can be therapeutically or prophylactically treated via a
 CC method of hydrolysing a lipid comprising expressing in a target cell or
 CC contacting a target cell with an effective amount of DNA or protein of
 CC the invention. Sequences AA083841-AA083897 represent Bacillus lipase
 CC polypeptides of the invention.
 XX
 SQ Sequence 212 AA;
 Query Match 97.5%; Score 1061; DB 23; Length 212;
 Best Local Similarity 98.1%; Pred. No. 9.4e-101;
 Matches 208; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MKFVKRRRIALVTIILSVTSLFAMOPSAKAAEHNPVNVVHIGASYNFAGIKSYLSQ 60
 DB 1 MKFVKRRRIALVTIILSVTSLFAMOPSAKAAEHNPVNVVHIGASYNFAGIKSYLSQ 60
 QY 61 GMSRGLYAVDFWMDKTGTNYNNGPVLSPFYQVLDGTGAKKVDYAHSMGANTPYRYKN 120
 DB 61 GMSRGLYAVDFWMDKTGTNYNNGPVLSPFYQVLDGTGAKKVDYAHSMGANTPYRYKN 120
 QY 121 LDGKNKIEENVVTLGGANRSTSKALPGTDPNOKIILYTSYSSADMTVMYLSKLDGAKNV 180
 DB 121 LDGKNKIEENVVTLGGANRSTSKALPGTDPNOKIILYTSYSSADMTVMYLSKLDGAKNV 180
 QY 181 QIHGVGHIGLNMNSQVNSLIKEGLNGGONTN 212
 DB 181 QIHGVGHIGLNMNSQVNSLIKEGLNGGONTN 212
 RESULT 5
 AA083845
 ID AA083845 standard; Protein; 212 AA.
 XX
 AC AA083845;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Bacillus lipase polypeptide #5.
 XX
 KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
 KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
 KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;

KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KM gastrointestinal lipid related condition; antiinflammatory; respiratory;
XX gastrointestnal.
OS Bacillus circulans.
XX W0200206457-A2.
XX 24-JAN-2002.
XX PD
XX PF 13-JUL-2001; 2001WO-US22160.
XX PR 13-JUL-2000; 2000US-217954P.
XX PR 21-JUN-2001; 2001US-300378P.
XX PA (MAXY-) MAXYGEN INC.
XX PI Glaver LJ, Minshull J, Vogel K;
XX DR WPI; 2002-171805/22.
XX DR N-PSDB; ABR33823.
XX PT Nucleic acids encoding lipase enzymes which are useful as supplements
PT in animal feeds, as agents of flavour modification and for treating
PT Crohn's disease and coeliac disease -
XX PS Claim 20; Page 139; 196pp; English.
XX CC The invention relates to new Bacillus lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AA083841-AA083897 represent Bacillus lipase
CC polypeptides of the invention.
XX SQ Sequence 212 AA;
SQ Query Match 97.4%; Score 1060; DB 23; Length 212;
Best Local Similarity 97.6%; Pred. No. 1.2e-100;
Matches 207; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
OY 1 MKFVKRRILAVTLIVSVTSLEFAMOPSAKAENHPVVMVHGIGASYNFAGIKSYLSQ 60
DB 1 MKFVKRRILAVTLIVSVTSLEFAMOPSAKAENHPVVMVHGIGASYNFAGIKSYLSQ 60
OY 61 GMSRGKLYAVDFMDKTGTNNYNGPVLSEFVOKVDETGAKKVDIVAHSMGANTPYIKN 120
DB 61 GMSRGKLYAVDFMDKTGTNNYNGPVLSEFVOKVDETGAKKVDIVAHSMGANTPYIKN 120
OY 121 LDGNGKLENNVTLGGANSTTSKALPGTDPNOKILLYTSIYSADMTVNNYLSKLDGAKNA 180
DB 121 LDGNGKLENNVTLGGANSTTSKALPGTDPNOKILLYTSIYSADMTVNNYLSKLDGAKNA 180
OY 181 QIHGVGHIGLIMNSOVNSLIKEGLNGGGOONTN 212
DB 181 QIHGVGHIGLIMNSOVNSLIKEGLNGGGOONTN 212
RESULT 6
AA083846
ID AA083846 standard; Protein: 212 AA.
XX AC AA083846;
XX DT 08-MAY-2002 (first entry)
XX XX

DE Bacillus lipase polypeptide #6.
XX XX
KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
XX gastrointestnal.
XX OS Bacillus azotofomans.
XX XX
XX PN W0200206457-A2.
XX PD 24-JAN-2002.
XX PF 13-JUL-2001; 2001WO-US22160.
XX PR 13-JUL-2000; 2000US-217954P.
XX PR 21-JUN-2001; 2001US-300378P.
XX PA (MAXY-) MAXYGEN INC.
XX PI Glaver LJ, Minshull J, Vogel K;
XX DR WPI; 2002-171805/22.
XX DR N-PSDB; ABR33824.
XX PT Nucleic acids encoding lipase enzymes which are useful as supplements
PT in animal feeds, as agents of flavour modification and for treating
PT Crohn's disease and coeliac disease -
XX PS Claim 20; Page 139; 196pp; English.
XX CC The invention relates to new Bacillus lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AA083841-AA083897 represent Bacillus lipase
CC polypeptides of the invention.
XX SQ Sequence 212 AA;
SQ Query Match 96.2%; Score 1047; DB 23; Length 212;
Best Local Similarity 96.7%; Pred. No. 2.6e-99;
Matches 205; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
OY 1 MKFVKRRILAVTLIVSVTSLEFAMOPSAKAENHPVVMVHGIGASYNFAGIKSYLSQ 60
DB 1 MKFVKRRILAVTLIVSVTSLEFAMOPSAKAENHPVVMVHGIGASYNFAGIKSYLSQ 60
OY 61 GMSRGKLYAVDFMDKTGTNNYNGPVLSEFVOKVDETGAKKVDIVAHSMGANTPYIKN 120
DB 61 GMSRGKLYAVDFMDKTGTNNYNGPVLSEFVOKVDETGAKKVDIVAHSMGANTPYIKN 120
OY 121 LDGNGKLENNVTLGGANSTTSKALPGTDPNOKILLYTSIYSADMTVNNYLSKLDGAKNA 180
DB 121 LDGNGKLENNVTLGGANSTTSKALPGTDPNOKILLYTSIYSADMTVNNYLSKLDGAKNA 180
OY 181 QIHGVGHIGLIMNSOVNSLIKEGLNGGGOONTN 212
DB 181 QIHGVGHIGLIMNSOVNSLIKEGLNGGGOONTN 212
RESULT 7
AA083849
ID AA083849 standard; Protein: 212 AA.

AA083849;
08-MAY-2002 (first entry)
Bacillus lipase polypeptide #9.
Lipase; Bacillus; animal feed; flavour modification; fat modification;
human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
gastrointestinal lipid related condition; antiinflammatory; respiratory;
gastrointestinal.
Bacillus sp.
WO200206457-A2.
24-JAN-2002.
13-JUL-2001; 2001WO-US22160.
13-JUL-2000; 2000US-217954P.
21-JUN-2001; 2001US-300378P.
(MAXY-) MAXYGEN INC.
Glaver LJ, Minshull J, Vogel K;
WPI: 2002-171805/22.
N-PSDB: ABR33827.
Nucleic acids encoding lipase enzymes which are useful as supplements
in animal feeds, as agents of flavour modification and for treating
Crohn's disease and coeliac disease -
Claim 32; Page 139; 196pp; English.
The invention relates to new Bacillus lipase enzymes and the nucleic
acids encoding them. The lipase polypeptides are useful as supplements in
animal feeds, as agents of flavour modification and fat modification in
human foodstuffs (e.g. cheese), as agents in the creation of food
emulsifiers, as agents for tanning/processing of leather and as cleaning
agents. They are also useful for treating Crohn's disease, cystic
fibrosis, coeliac disease, indigestion, obesity and other
gastrointestinal mal-absorption problems. Gastrointestinal lipid related
conditions can be therapeutically or prophylactically treated via a
method of hydrolysing a lipid comprising expressing in a target cell or
contacting a target cell with an effective amount of DNA or protein of
the invention. Sequences AA083841-AA083857 represent Bacillus lipase
polypeptides of the invention.

	Query Match	92.6%.	Score 1008:	DB 23;	Length 212:	
	Best Local Similarity	92.9%.	Pred. No.2.6e-95:			
	Matches 197:	Conservative 7;	Mismatches 6;	Indels 0;	Gaps 0;	
QY	1 MKFVKRRILAVTLTLLSVLSLFAMOPSAKAENHPVVMVHIGAGSYNFAGIKSYLSQ	60				
Db	1 MKFVKRRILAVTLTLLSVLSLFALQPASAKAENHPVVMVHIGAGSFNFAIKSYLSQ	60				
QY	61 GMSRCKLAVDPFMDKTGNTNNNGPVLSPFYOKVLDDETAKKVDIYAHSKGNANTYYIKN	120				
Db	61 GMSRCKLAVDPFKDTGTGNTNNNGPVLSPFYOKVLDDETAKKVDIYAHSKGNANTYYIKN	120				
QY	121 LDGSKRIENVVTLLGKANSTSKALPGDPPPOKILYTYSADAMYIVANNYLKLGDGAIA	180				
Db	121 LDGSKRIENVVTLLGKANLTITGKALPGDPPPOKILYTYSADAMIVANNYLRLDGARNV	180				
QY	181 QIHGVGHIGLLMNSOVNSLIKEGLNGGGQNTN	212				
Db	181 QIHGVGHIGLLYSSOVNSLIKEGLNGGGGLNTN	212				

```

XX RESULT 8
AC AAU83842 ID AAU83842 standard; Protein: 212 AA.
XX
XX AAU83842;
XX
XX 08-MAY-2002 (first entry)
XX DE
XX Bacillus lipase polypeptide #2.
XX
XX Lipase: Bacillus; animal feed; flavour modification; fat modification;
XX human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
XX leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
XX coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
XX gastrointestinal lipid related condition; antiinflammatory; respiratory;
XX gastrointestinal.
XX
XX Bacillus subtilis.
XX OS
XX WO200206457-A2.
XX PN
XX PD 24-JAN-2002.
XX XX
XX PF 13-JUL-2001; 2001WO-US22160.
XX PR 13-JUL-2000; 2000US-217954P.
XX PR 21-JUN-2001; 2001US-300378P.
XX PA (MAXY-) MAXGEN INC.
XX
XX Glver LJ, Minshull J, Vogel K;
XX P1 WPI: 2002-171805/22.
XX DR 'N-PSDB; ABK33820.
XX
XX Nucleic acids encoding lipase enzymes which are useful as supplements
XX PT in animal feeds, as agents of flavour modification and for treating
XX FT Crohn's disease and coeliac disease -
XX PS
XX Claim 38; Page 138; 196pp; English.
XX
XX The invention relates to new Bacillus lipase enzymes and the nucleic
XX CC acids encoding them. The lipase polypeptides are useful as supplements in
XX CC animal feeds, as agents of flavour modification and fat modification in
XX CC human foodstuffs (e.g. cheese), as agents in the creation of food
XX CC emulsifiers, as agents for tanning/processing of leather and as cleaning
XX CC agents. They are also useful for treating Crohn's disease, cystic
XX CC fibrosis, coeliac disease, indigestion, obesity and other
XX CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
XX CC conditions can be therapeutically or prophylactically treated via a
XX CC method of hydrolysing a lipid comprising expressing in a target cell or
XX CC contacting a target cell with an effective amount of DNA or protein of
XX CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
XX CC polypeptides of the invention.
XX
XX Sequence 212 AA:
XX
XX Query Match 92.6%, Score 1007, DB 23; Length 212;
XX Best Local Similarity 92.0%; Pred. No. 3.3e-95;
XX Matches 195; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
XX
XX 1 MKPKARRIATVTLIVLSLTFAMQPSAKAAEHNPVMVHIGGASVNFGRISLVSQ 60
XX 1 MKFKARRIATVTLIMLSVSLFLAPSPAKAAEHPVAVMVBHGIGASFNFPAIKSYLVSO 60
XX Db 1 MKFKARRIATVTLIMLSVSLFLAPSPAKAAEHPVAVMVBHGIGASFNFPAIKSYLVSO 60
XX
XX 61 GMSRGLTVAVDPMWKTGTNYNNGPVLSFPPVOKVLDETGAKKVDIAHSMGANGAPPYYTKN 120
XX 61 GMSRGLTVAVDPMWKTGTNYNNGPVLPFRFOVKVLDDETGAKKVDIAHSMGANTLYTIKN 120
XX Db 61 GMSRGLTVAVDPMWKTGTNYNNGPVLPFRFOVKVLDDETGAKKVDIAHSMGANTLYTIKN 120
XX
XX 121 LDGGKRIENVVTLLGANSTTSKALPGCDPMOKILTYITSADMTVMNTYLSKLDAKNA 180
XX 121 LDGGKRIENVVTLLGANSTTSKALPGCDPMOKILTYITSADMTVMNTYLSKLDAKNA 180
XX 121 LDGGKRIENVVTLLGANSTTSKALPGCDPMOKILTYITSADMTVMNTYLSKLDAKNA 180

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Qy 1 MKFVKRRRIALVTILVSLVTSLEFAMQPSAKAAEHNPVWVHGIGASYNFAGIKSYLSQ 60
 Db 1 MKFVKRRRIALVTILVSLVTSLEFALQPSAKAAEHNPVWVHGIGASYNFAGIKSYLSQ 60
 Qy 61 GMSRCKLVAVDWDKGTGTNNNGPVLRSFYQVLDFTGAKKVDIYAHSGGANTPYIYN 120
 Db 61 GMSRCKLVAVDWDKGTGNLNGPVLRSFYKVLDETGAKKVDIYAHSGGANTLYIYN 120
 Qy 121 LDGKNKIEENVVTLGGANRSTSKALPGTDPNOKILYTSYSSADMTVMYLSKLDGAKNA 180
 Db 121 LDGKNKIEENVVTLGGANRLVLTGKALPGTDPNOKILYTSYSSADMTVMYLSKLDGAKNV 180
 Qy 181 QIHGVGHIGLLMNSOVNSLKEGNGGCGNTN 212
 Db 181 QIHGVGHIGLLYSQVNSLKEGNGGGLNTN 212

RESULT 11
 AAU83856 standard; Protein: 212 AA.
 AC AAU83856;
 DT 08-MAY-2002 (first entry)
 DE Bacillus lipase polypeptide #16.
 KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
 KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
 KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
 KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
 KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
 KW gastrointestinal.
 OS Bacillus sp.
 PN WO200206457-A2.
 PD 24-JAN-2002.
 PF 13-JUL-2001; 2001WO-US22160.
 PR 13-JUL-2000; 2000US-217954P.
 PR 21-JUN-2001; 2001US-300378P.
 PA (MAXY-) MAXYGEN INC.
 PI Giver LJ, Minshull J, Vogel K;
 DR WPI: 2002-171805/22.
 DR N-PSDB: ABR33834.
 PT Nucleic acids encoding lipase enzymes which are useful as supplements
 PT in animal feeds, as agents of flavour modification and for treating
 PT Crohn's disease and coeliac disease -
 PS Claim 32; Page 140; 196pp; English.
 CC The invention relates to new Bacillus lipase enzymes and the nucleic
 CC acids encoding them. The lipase polypeptides are useful as supplements in
 CC animal feeds, as agents of flavour modification and fat modification in
 CC human foodstuffs (e.g. cheese), as agents in the creation of food
 CC emulsifiers, as agents for tanning/processing of leather and as cleaning
 CC agents. They are also useful for treating Crohn's disease, cystic
 CC fibrosis, coeliac disease, indigestion, obesity and other
 CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
 CC conditions can be therapeutically or prophylactically treated via a
 CC method of hydrolysing a lipid comprising expressing in a target cell or
 CC contacting a target cell with an effective amount of DNA or protein of
 CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
 CC polypeptides of the invention.
 CC Sequence 212 AA:
 SO

Query Match 91.2%; Score 992; DB 23; Length 212;
 Best Local Similarity 92.0%; Pred No. 1.2e-93;
 Matches 195; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MKFVKRRRIALVTILVSLVTSLEFAMQPSAKAAEHNPVWVHGIGASYNFAGIKSYLSQ 60
 Db 1 MKFVKRRRIALVTILVSLVTSLEFALQPSAKAAEHNPVWVHGIGASYNFAGIKSYLSQ 60
 Qy 61 GMSRCKLVAVDWDKGTGTNNNGPVLRSFYQVLDFTGAKKVDIYAHSGGANTPYIYN 120
 Db 61 GMSRCKLVAVDWDKGTGNLNGPVLRSFYKVLDETGAKKVDIYAHSGGANTLYIYN 120
 Qy 121 LDGKNKIEENVVTLGGANRSTSKALPGTDPNOKILYTSYSSADMTVMYLSKLDGAKNA 180
 Db 121 LDGKNKIEENVVTLGGANRLVLTGKALPGTDPNOKILYTSYSSADMTVMYLSKLDGAKNV 180
 Qy 181 QIHGVGHIGLLMNSOVNSLKEGNGGCGNTN 212
 Db 181 QIHGVGHIGLLYSQVNSLKEGNGGGLNTN 212

RESULT 12
 AAU83854 standard; Protein: 212 AA.
 AC AAU83854;
 DT 08-MAY-2002 (first entry)
 DE Bacillus lipase polypeptide #14.
 KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
 KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
 KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
 KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
 KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
 KW gastrointestinal.
 OS Bacillus sp.
 PN WO200206457-A2.
 PD 24-JAN-2002.
 PF 13-JUL-2001; 2001WO-US22160.
 PR 13-JUL-2000; 2000US-217954P.
 PR 21-JUN-2001; 2001US-300378P.
 PA (MAXY-) MAXYGEN INC.
 PI Giver LJ, Minshull J, Vogel K;
 DR WPI: 2002-171805/22.
 DR N-PSDB: ABR33832.
 PT Nucleic acids encoding lipase enzymes which are useful as supplements
 PT in animal feeds, as agents of flavour modification and for treating
 PT Crohn's disease and coeliac disease -
 PS Claim 30; Page 140; 196pp; English.
 CC The invention relates to new Bacillus lipase enzymes and the nucleic
 CC acids encoding them. The lipase polypeptides are useful as supplements in
 CC animal feeds, as agents of flavour modification and fat modification in
 CC human foodstuffs (e.g. cheese), as agents in the creation of food
 CC emulsifiers, as agents for tanning/processing of leather and as cleaning
 CC agents. They are also useful for treating Crohn's disease, cystic
 CC fibrosis, coeliac disease, indigestion, obesity and other
 CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
 CC conditions can be therapeutically or prophylactically treated via a
 CC method of hydrolysing a lipid comprising expressing in a target cell or

CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AA083841-AA083897 represent Bacillus lipase
CC polypeptides of the invention.

SO Sequence 212 AA;

Query Match 90.9%; Score 989; DB 23; Length 212;
Best Local Similarity 91.5%; Pred. No. 2,4e-93;
Matches 194; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 MKFVRRRIIAVLTVLVTSLFAQPSAKAEHNPVVMVHIGGASYNFAGIKSYLSQ 60
DB 1 MKFVRRRIIAVLTVLVTSLFAQPSAKAEHNPVVMVHIGGASYNFAGIKSYLSQ 60
QY 61 GMSRCKLYAVDFWMDKTGYNNGPVLNRFVQVLDGTGAKKVDIVAHSMGANTPYITKN 120
DB 61 GMSRCKLYAVDFWMDKTGYNNGPVLNRFVQVLDGTGAKKVDIVAHSMGANTPYITKN 120
QY 121 LDGSKKINNVVTLGGANRSTSKALPGTDPNOKILYTSYSSADMIVMNYLTKLDGAKNV 180
DB 121 LDGSKKINNVVTLGGANRSTSKALPGTDPNOKILYTSYSSADMIVMNYLTKLDGAKNV 180
QY 181 QIHGVGHIGLMSQVNSLIKEGLNGGQNTN 212
DB 181 QIHGVGHIGLMSQVNSLIKEGLNGGQNTN 212

RESULT 13

AA083894
ID AA083894 standard; Protein: 180 AA.

AC AA083894;

DT 08-MAY-2002 (first entry)

DE Bacillus lipase polypeptide #54.

lipase; Bacillus; animal feed; flavour modification; fat modification;
human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
gastrointestinal lipid related condition; antiinflammatory; respiratory;
gastrointestinal.

OS Synthetic.

PN WO200206457-A2.

PD 24-JAN-2002.

PF 13-JUL-2001; 2001WO-US22160.

PR 13-JUL-2000; 2000US-217954P.

PR 21-JUN-2001; 2001US-300378P.

PA (MAXY-) MAXYGEN INC.

PI Giver LJ, Minshull J, Vogel K;

PI WPI; 2002-171805/22.

DR N-PSDB; ABR33872.

PT Nucleic acids encoding lipase enzymes which are useful as supplements

PT in animal feeds, as agents of flavour modification and for treating

PT Crohn's disease and coeliac disease -

PS Claim 5; Page 145-146; 196pp; English.

CC The invention relates to new Bacillus lipase enzymes and the nucleic

CC acids encoding them. The lipase polypeptides are useful as supplements in

CC animal feeds, as agents of flavour modification and fat modification in

CC human foodstuffs (e.g. cheese), as agents in the creation of food

CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AA083841-AA083897 represent Bacillus lipase
CC polypeptides of the invention.

SO Sequence 180 AA;

Query Match 85.0%; Score 925; DB 23; Length 180;
Best Local Similarity 90.3%; Pred. No. 7e-87;
Matches 177; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 33 EHNPPVVMVHIGGASYNFAGIKSYLSVSGMSRGLYAVDFMDKTGTYNNNGPVLNRFVQK 92
DB 1 EHNPPVVMVHIGGASYNFAGIKSYLSVSGMSRGLYAVDFMDKTGTYNNNGPVLNRFVQK 92
QY 93 VLDETGAARKVDIVAHSMGANTPYITKNLDGSKKINNVVTLGGANRSTSKALPGTDPNQ 152
DB 93 VLDETGAARKVDIVAHSMGANTPYITKNLDGSKKINNVVTLGGANRSTSKALPGTDPNQ 152
QY 153 KILYTSYSSADMIVMNYLTKLDGAKNVQIHGVGHIGLMSQVNSLIKEGLNGGQNTN 212
DB 121 KILYTSYSSADMIVMNYLTKLDGAKNVQIHGVGHIGLMSQVNSLIKEGLNGGQNTN 212

RESULT 14

AA083890
ID AA083890 standard; Protein: 180 AA.

AC AA083890;

DT 08-MAY-2002 (first entry)

DE Bacillus lipase polypeptide #50.

lipase; Bacillus; animal feed; flavour modification; fat modification;
human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
gastrointestinal lipid related condition; antiinflammatory; respiratory;
gastrointestinal.

OS Synthetic.

PN WO200206457-A2.

PD 24-JAN-2002.

PF 13-JUL-2001; 2001WO-US22160.

PR 13-JUL-2000; 2000US-217954P.

PR 21-JUN-2001; 2001US-300378P.

PA (MAXY-) MAXYGEN INC.

PI Giver LJ, Minshull J, Vogel K;

PI WPI; 2002-171805/22.

DR N-PSDB; ABR33868.

PT Nucleic acids encoding lipase enzymes which are useful as supplements

PT in animal feeds, as agents of flavour modification and for treating

PT Crohn's disease and coeliac disease -

PS Claim 5; Page 145; 196pp; English.

CC The invention relates to new Bacillus lipase enzymes and the nucleic

CC acids encoding them. The lipase polypeptides are useful as supplements in

CC animal feeds, as agents of flavour modification and fat modification in

CC human foodstuffs (e.g. cheese), as agents in the creation of food

CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
CC polypeptides of the invention.

SQ Sequence 180 AA:

Query Match

Best Local Similarity 97.8%; Score 921; DB 23; Length 180;

Matches 176; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 33 EHNPPVVMVHGIGASYNFAGIKSYLVSOGRKLYAVDFWDXGTGTYNNGPVLSPRVOK 92
DB 1 EHNPPVVMVHGIGASYNFAGIKSYLVSOGRKLYAVDFWDXGTGTYNNGPVLSPRVOK 60
OY 93 VLDGTGAKKVDIVAHSMGANTPYITKNDGKKIENVVTLGGANSTTSKALPGTDPNQ 152
DB 61 VLDGTGAKKVDIVAHSMGANTLYITKNDGKKIENVVTLGGANSTTSKALPGTDPNQ 120
OY 153 KILYTSYSSADMIVMNYLSKLDGAKNAQIHGVGHIGLLMNSOVNSLIKEGLNGGGONTN 212
DB 121 KILYTSYSSADMIVMNYLSKLDGAKNAQIHGVGHIGLLMNSOVNSLIKEGLNGGGONTN 180

RESULT 15

AAU83884
ID AAU83884 standard; Protein; 180 AA.

AC AAU83884;

DT 08-MAY-2002 (first entry)

DE Bacillus lipase polypeptide #44.

KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuff; cheese; food emulsifier; leather tanning; enzyme;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
KW gastrointestinal.

OS Synthetic.

PN WO200206457-A2.

PD 24-JAN-2002.

PF 13-JUL-2001; 2001WO-US22160.

PR 13-JUL-2000; 2000US-217954P.

PR 21-JUN-2001; 2001US-300378P.

PA (MAXY-) MAXYGEN INC.

PI Giver LJ, Minshall J, Vogel K;

DR WPI; 2002-171805/22.

DR N-PSDB; ABR33862.

PT Nucleic acids encoding lipase enzymes which are useful as supplements
PT in animal feeds, as agents of flavour modification and for treating
PT Crohn's disease and coeliac disease -

PS Claim 5; Page 144; 196pp; English.

CC The invention relates to new Bacillus lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in

CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences AAU83841-AAU83897 represent Bacillus lipase
CC polypeptides of the invention.

SQ Sequence 180 AA:

Query Match

Best Local Similarity 97.2%; Score 918; DB 23; Length 180;

Matches 175; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 33 EHNPPVVMVHGIGASYNFAGIKSYLVSOGRKLYAVDFWDXGTGTYNNGPVLSPRVOK 92
DB 1 EHNPPVVMVHGIGASYNFAGIKSYLVSOGRKLYAVDFWDXGTGTYNNGPVLSPRVOK 60
OY 93 VLDGTGAKKVDIVAHSMGANTPYITKNDGKKIENVVTLGGANSTTSKALPGTDPNQ 152
DB 61 VLDGTGAKKVDIVAHSMGANTLYITKNDGKKIENVVTLGGANSTTSKALPGTDPNQ 120
OY 153 KILYTSYSSADMIVMNYLSKLDGAKNAQIHGVGHIGLLMNSOVNSLIKEGLNGGGONTN 212
DB 121 KILYTSYSSADMIVMNYLSKLDGAKNAQIHGVGHIGLLMNSOVNSLIKEGLNGGGONTN 180

Search completed: May 9, 2003, 16:20:58

Job time : 36 secs

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OM protein - protein search, using sw model

Run on: May 9, 2003, 16:20:26 ; Search time 14 Seconds
(without alignments)
445.547 Million cell updates/sec

Title: US-09-905-666A-55
Perfect score: 1088
Sequence: 1 MKFVKRRRIALVTILVLSVT.....NSQVNSLIKEGLNGCGONTN 212

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	798.5	73.4	213	1 US-07-930-678-2	Sequence 2, Appli
2	139.5	12.8	358	1 US-08-034-650-10	Sequence 10, Appl
3	139.5	12.8	358	1 US-08-449-015-10	Sequence 10, Appl
4	123	11.3	363	3 US-08-978-589A-2	Sequence 2, Appli
5	122	11.2	363	4 US-09-336-601-1	Sequence 1, Appli
6	114	10.5	364	1 US-08-400-422-3	Sequence 3, Appli
7	97.5	9.0	292	4 US-09-134-001C-3301	Sequence 3301, Ap
8	92	8.5	699	4 US-09-134-001C-4054	Sequence 4054, Ap
9	91.5	8.4	690	4 US-09-134-001C-4568	Sequence 4568, Ap
10	88	8.1	213	1 US-08-104-445-3	Sequence 3, Appli
11	87.5	8.0	313	3 US-08-732-412-2	Sequence 2, Appli
12	87.5	8.0	388	1 US-08-232-519-2	Sequence 2, Appli
13	87.5	8.0	388	1 US-08-456-956-2	Sequence 2, Appli
14	87	8.0	652	4 US-09-134-001C-3517	Sequence 3517, Ap
15	86.5	8.0	277	3 US-09-111-556A-3	Sequence 3, Appli
16	86.5	8.0	277	3 US-08-360-758-3	Sequence 3, Appli
17	86	7.9	535	3 US-08-286-870A-6	Sequence 6, Appli
18	86	7.9	648	3 US-08-286-870A-4	Sequence 4, Appli
19	86	7.9	719	3 US-08-286-870A-8	Sequence 8, Appli
20	85	7.8	262	2 US-08-602-359A-35	Sequence 35, Appli
21	85	7.8	3729	2 US-08-804-227C-4	Sequence 4, Appli
22	83.5	7.7	264	4 US-09-134-001C-5592	Sequence 5592, Ap
23	82.5	7.6	640	4 US-09-509-814A-6	Sequence 6, Appli
24	82.5	7.6	640	4 US-09-509-814A-8	Sequence 8, Appli
25	82	7.5	178	1 US-08-044-621D-32	Sequence 32, Appli
26	82	7.5	178	1 US-08-709-912-15	Sequence 15, Appli
27	82	7.5	178	2 US-09-047-370-15	Sequence 15, Appli

28	82	7.5	671	2 US-08-737-716-13	Sequence 13, Appli
29	81.5	7.5	275	6 5472855-5	Patent No. 5472855
30	81.5	7.5	551	4 US-09-615-192A-348	Sequence 348, App
31	81	7.4	312	4 US-09-134-001C-3465	Sequence 3465, Ap
32	81	7.4	1073	4 US-09-206-942-49	Sequence 49, Appli
33	81	7.4	1079	4 US-09-206-942-47	Sequence 47, Appli
34	80.5	7.4	284	4 US-09-134-001C-2927	Sequence 2927, Ap
35	80	7.4	316	1 US-07-828-980A-2	Sequence 2, Appli
36	80	7.4	539	4 US-09-036-987A-11	Sequence 11, Appli
37	80	7.4	539	4 US-09-370-700-11	Sequence 11, Appli
38	78.5	7.2	1426	4 US-09-136-574A-43	Sequence 43, Appli
39	78	7.2	340	4 US-09-134-001C-4056	Sequence 4056, Ap
40	78	7.2	366	4 US-09-134-001C-4412	Sequence 4412, Ap
41	78	7.2	371	3 US-08/622	INFORMATION FOR
42	78	7.2	371	4 US-09-165-922A-10	Sequence 10, Appli
43	78	7.2	503	4 US-09-562-737-64	Sequence 64, Appli
44	78	7.2	1104	4 US-09-268-347-28	Sequence 28, Appli
45	78	7.2	1104	4 US-09-268-347-34	Sequence 34, Appli

ALIGNMENTS

RESULT 1
US-07-930-678-2
Sequence 2, Application US/07930678
Patent No. 5427936
GENERAL INFORMATION:
APPLICANT: MOELLER, Bernhard
APPLICANT: VETTER, Roman
APPLICANT: WILKE, Detlef
APPLICANT: FOULLOIS, Birgit
TITLE OF INVENTION: Alkaline Bacillus Lipases, Coding DNA
TITLE OF INVENTION: Sequences therefor and Bacilli, Which produce these
TITLE OF INVENTION: Lipases
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/930,678
FILING DATE: 19921013
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP91/00664
FILING DATE: 08-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 40 12 070.8
FILING DATE: 14-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, J.D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 16877/318/KACH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-930-678-2

Query Match	73.4%;	Score 798.5;	DB 1;	Length 213;
Best Local Similarity	73.9%;	Pred. No. 3.7e-79;		
Matches 156; Conservative	22;	Mismatches 32;	Indels 1;	Gaps 1

[illegible]

RESULT

```

US-08-034-650-10
Sequence 10, Application US/08034650
Patent No. 5641671
GENERAL INFORMATION:
APPLICANT: BOS, Jannetje W.
APPLICANT: FRENKEN, Leon G.
APPLICANT: VERRIPS, Cornelis T.
APPLICANT: VISSER, Christiaan
TITLE OF INVENTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUTAMATE
TITLE OF INVENTION: LIPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1615 L. Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/034,650
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/727,235
FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kokulis, Paul N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: PNK/5970/91731
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEO ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-034-650-10

```

Query Match	12.8%;	Score 139.5;	DB 1;	Length 358;
Best Local Similarity	29.6%;	Pred. No. 5.6e-07;		
Matches	48;	Conservative	26;	Mismatches 59;
			Indels	29;
			Gaps	8;

```

QY      1 MKFKARRIALVTLVLTLSVLSL-----FMQCSAAAE-----NHPVVMHIGCASY 48
      . 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      2 VRSMKSRVRAARAIVAMALAVMPLAGLGTMAAPAAVAADTYATRYPVILVHGLAGTD- 60

QY      49 NEA-----GIRKVLVSGSGSRGKTLAVD---FMQDTGNNNGPVLSFSGVLDKETS 98
      . 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db      61 KFAVNVDPVWYIGSDLSHG---AKVYVANIISGQSDGPR-GAGEBOLLAVYKQVLAATG 116

QY      99 AKKVDIVAHSMGAGANTPYIKINLDGSKNIENVTLGGANST. 140
      . 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db     117 ATKVNLIGHSGGLTSRIYA--AVAPOLVAVSYTITGPHRKS 156 ;

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RESULT 3
US-08-449-015-10

```

1 Sequence 10, Application US/08449015
2 Patent No. 5804409
3
4 GENERAL INFORMATION:
5 APPLICANT: BOS, Jannetje W.
6 APPLICANT: FREKKEN, Leon G.
7 APPLICANT: VERRIPS, Cornelis T.
8 APPLICANT: VISSER, Christiaan
9 TITLE OF INVENTION: PRODUCTION OF ACTIVE PSEUDOMONAS GLUAMAE
10 TITLE OF INVENTION: LIPASE IN HOMOLOGOUS OR HETEROLOGOUS HOSTS
11 NUMBER OF SEQUENCES: 13
12 CORRESPONDENCE ADDRESS:
13 ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
14 STREET: 1615 L. Street, N.W.
15 CITY: Washington
16 STATE: D.C.
17 COUNTRY: USA
18 ZIP: 20036-5601
19
20 COMPUTER READABLE FORM:
21
22 MEDIUM TYPE: Floppy disk
23
24 COMPUTER: IBM PC compatible
25 OPERATING SYSTEM: PC-DOS/MS-DOS
26 SOFTWARE: PatentIn Release #1.0, Version #1.25
27
28 CURRENT APPLICATION DATA:
29 APPLICATION NUMBER: US/08/449,015
30 FILING DATE: 24-MAY-1995
31 CLASSIFICATION: 435
32
33 PRIOR APPLICATION DATA:
34 APPLICATION NUMBER: US 07/727,235
35 FILING DATE: 03-JUL-1991
36
37 ATTORNEY/AGENT INFORMATION:
38 NAME: Kokulis, Paul N.
39 REGISTRATION NUMBER: 16,773
40 REFERENCE/DOCKET NUMBER: PNK/5970/91731
41
42 TELECOMMUNICATION INFORMATION:
43 TELEPHONE: (202) 861-3000
44 TELEFAX: (202) 822-0944
45
46 TELEX: 6714627 CUSH
47
48 INFORMATION FOR SEQ ID NO: 10:
49 SEQUENCE CHARACTERISTICS:
50 LENGTH: 358 amino acids
51 TYPE: amino-acid
52 TOPOLOGY: Linear
53
54 MOLECULE TYPE: protein
55
56 US-08-449-015-10

```

Query Match	12.8%	Score 139.5	DB 1	Length 358
Best Local Similarity	29.6%	Pred. No. 5.6e-07		
Matches 48	Conservative 26	Mismatches 59	Indels 29	Gaps 8

```

OY      1  MKFKRRRLALVTLLVLSVSL-----FMQPSAAAE-----NRPVVMHGIGASY 48
Db      2  VRSNRSRRAARAAYAMALALVMPPLAGAGLTMAASPAAYAAOTYATRRPVLTVHGAGTD- 60

OY      49  NFA-----GKISLYLSQGSRRCKLLAYD---FWMDTGTNTNNNGPLSLSFQVQKVIDETG 98
Db      61  KFAANVDWYVYISQSDLDOSHG---AKVYVIANISGFQSDSDGPN-GRGEOLLAYVKQVLAATG 116

OY      99  AKKVDIVAHSMGSGANTPYIYIKLNLDGKRIENYVTLGGANST 140

```

Db 117 ATKVNLHSGGLTSRYVA--AVAPOLVASVTITGTHRGCS 156

RESULT 4
US-08-978-589A-2
Sequence 2, Application US/08978589A
Patent No. 6087145

GENERAL INFORMATION:

APPLICANT: ISHII, Takeshi

APPLICANT: MITSUDA, Satoshi

TITLE OF INVENTION: ESTERASE GENE AND ITS USE

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP

STREET: P.O. BOX 747

CITY: FALLS CHURCH

STATE: VIRGINIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 22040

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/978,589A

FILING DATE: 26-NOV-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Murphy Jr., Gerald M.

REGISTRATION NUMBER: 28,977

REFERENCE/DOCKET NUMBER: 20-4336P

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 205-8000

TELEFAX: (703) 205-8050

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 363 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-978-589A-2

Query Match

Best Local Similarity 27.0%; Score 123; DB 3; Length 363;

Matches 43; Conservative 27; Mismatches 59; Indels 30; Gaps 9;

Db 13 TILVLSVTSLFAMQPSAK-----AAEHNPVYVNHGIGASYNFAGIKSYLSQGSRR--- 64

Db 26 TVLWMSLAGAQAASATAVDDYATRYPIILVHGLTGTD-KYGGVVEY-----WYRIPE 79

Qy 65 -----GKLYAVD---FMDKGTNNNGPVLRSFYQKVLDETGAKKVDIVAHSGKANTP 115

Db 80 DIRAHGAAYVYANLSGFOSDDGPN-GRGEQLAFVKQYLAATGAOKVNLHSGGL-TS 137

Qy 116 YIRKNDGKNIENVTLG-----GANRSTTSKALPGTDP 150

Db 138 RYVASV-APELVASVTITSTPHWGSQFADFVQQLLOTDP 175

RESULT 5

US-09-336-601-1

Sequence 1, Application US/09336601

Patent No. 6184008

GENERAL INFORMATION:

APPLICANT: OHTA, Hiromichi

APPLICANT: SUGAI, Takeshi

APPLICANT: ISHII, Takeshi

APPLICANT: MITSUDA, Satoshi

TITLE OF INVENTION: PRODUCTION OF OPTICALLY ACTIVE SPHINGOID COMPOUND

FILE REFERENCE: 2185-349P

CURRENT APPLICATION NUMBER: US/09/336,601

CURRENT FILING DATE: 1999-06-21

EARLIER APPLICATION NUMBER: 09/034,007

EARLIER FILING DATE: 1998-03-03

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 363

TYPE: PRT

ORGANISM: E. coli JM 109/pAL 612 strain

US-09-336-601-1

Query Match

Best Local Similarity 11.2%; Score 122; DB 4; Length 363;

Matches 45; Conservative 32; Mismatches 61; Indels 42; Gaps 10;

Qy 4 VKRRILATVTLV-----SVTSLFAMQPSAK-----AAEHNPVYVNHGIGCA 46

Db 5 IRKAVATVVAIAMAAPAASVTVLSLAGAQAASATAVDDYATRYPIILVHGLTGT 64

Qy 47 SYNFAGIKSYLSQGSRR-----GKLYAVD---FMDKGTNNNGPVLRSFYQKVL 94

Db 65 D-KYGGVVEY-----WYRIPELRAHGAAYVYANLSGFOSDDGPN-GRGEQLAFVKQYL 117

Qy 95 DETGAKKVDIVAHSGKANTPYIRKNDGKNIENVTLG-----GANRSTTSKALPGTDP 150

Db 118 AATGAOKVNLHSGGL-TSRYVASV-APELVASVTITSTPHWGSQFADFVQQLLOTDP 175

RESULT 6

US-08-400-422-3

Sequence 3, Application US/08400422

Patent No. 5681715

GENERAL INFORMATION:

APPLICANT: Jorgensen, Steen Troels

APPLICANT: Diderichsen, Boerge Krag

APPLICANT: Buckley, Catherine M.

APPLICANT: Hobson, Audrey

APPLICANT: McConnell, David J.

TITLE OF INVENTION: A process for the preparation of an active

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 56817150 No. 5681715disk of No. 5681715th America, Inc.

STREET: 405 Lexington Avenue, 62nd floor

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10174-6201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/400,422

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/038,763

FILING DATE: 25-MAR-1993

APPLICATION NUMBER: PCT/DK91/00402

FILING DATE: 20-DEC-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/DK92/00391

FILING DATE: 18-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: Lambiris, Elias J.

REGISTRATION NUMBER: 33,728

REFERENCE/DOCKET NUMBER: 3663,200-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212 867 0123

TELEFAX: 212 867 0298

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 364 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Pseudomonas cepacia
STRAIN: DSM 3401
US-08-400-422-3

Query Match 10.5%; Score 114; DB 1; Length 364;
Best Local Similarity 25.9%; Pred. No. 0.00035;
Matches 42; Conservative 27; Mismatches 59; Indels 34; Gaps 8;

OY 4 VKRIIALVTLVLSV-----TSLFAMOPSAKAEH-----NPVVMHGIGGA 46
DB 5 MRSRVVAGAAVACAMSVAPFAGATAVMTLATTHAAMATAPDDYATRRYPILVHGLGT 64
OY 47 SYNFAGISKY-----LVSGMSRGLYAVD---FMDKTSTNNNGPVLSPFYOKVLDE 96
DB 65 D-KYAGVLEWYGIQEDLQOHG---ATVYVANLSGFQSDGPN-GRGEQLATVYKTVLAA 119
OY 97 TGAKKVDIVAHSMGAMTPYIKMLDGNKIENVYTLGGANR 138
DB 120 TGATKVNILVGHXGGLTSRYVA--AVAPDLVAVSTTGTGTPHR 159

RESULT 7
US-09-134-001C-3301
Sequence 3301, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3301
LENGTH: 292
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3301

Query Match 9.0%; Score 97.5; DB 4; Length 292;
Best Local Similarity 19.9%; Pred. No. 0.016;
Matches 48; Conservative 38; Mismatches 90; Indels 65; Gaps 9;

OY 13 TILVLSV-----TSLFAMOPSAKAEHNPVVMHGIGGASYNFAGIKSYLVSGW--- 62
DB 20 TVLVLIIVNKTOSQSYISTHYSNNKIKTTATLFLHGGGSESS---ETFMVQALNKN 75
OY 63 -----SRGKLY-----AVDFMD-KITGNNNGPVLSPFYOKVLDE 96
DB 76 VTNEVITARVSSEKGVFDRKLSDDAANPIYKVEFKDKNGKFNEMVWIKEVLSQLKSQ 135
OY 97 TGAKKVDIVAHSMGAMTPYIKMLDGN---KIENVYTLGG-----ANRSTTS 142
DB 136 FGIOGFNFVGHSMKNISFATFMKRYGDDRHLPOLAKEVYNAGVYNGILNMENVEIIVD 195
OY 143 KALPGTDPN---OKILYTSIYSSADMIVMNYLSKLDGAKNAQIHGVGHIGLILNNSOVNS 198
DB 196 KGGPRSMNAAYRQLLSLYKTYCGKEIEVLNIYGDLEDGSHSD-----GRVSNSSSQS 248

OY 199 L 199
DB 249 L 249

RESULT 8
US-09-134-001C-4054
Sequence 4054, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4054
LENGTH: 699
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4054

Query Match 8.5%; Score 92; DB 4; Length 699;
Best Local Similarity 19.7%; Pred. No. 0.23;
Matches 46; Conservative 37; Mismatches 60; Indels 90; Gaps 11;

OY 28 SAKAEH---NPVVMHGIGGASYNFAGIKSYLVSGWSRGL-----YAVD 71
DB 312 SAKOKYKNNPILVHGFNGETDD---INPSVLTHWGGDKMIRKODLENGYEAVEAS 368
OY 72 FMDKTSTNNNGPVLSPFYOKVLDEGTA-----KKVDIVA 106
DB 369 I-SAFGSYDAVAVLLYIKGRVDYGAHAHAKYGERYKTYGGYKWKPKGKIHILH 427
OY 107 HSMGAMTPYIKMLD-----GG--KNIENVYTLGGANR 138
DB 428 HSMGCT---IROLEELRHGNPEVEYOKOHGEISPLFGGHDNMVSSITTLGTPHN 483
OY 139 STSKALPGTDPNOKILYTSIYSSADMIVMNYLSKLDGAKNAQI-HGVGHIGL 190
DB 484 GTHASDLG---NEAIVRQLAVD-----VCKMGNKDSRVDFGLEHWGL 524

RESULT 9
US-09-134-001C-4568
Sequence 4568, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4568
LENGTH: 690
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4568

Query Match 8.4%; Score 91.5; DB 4; Length 690;
Best Local Similarity 20.4%; Pred. No. 0.26;
Matches 54; Conservative 32; Mismatches 72; Indels 107; Gaps 12;

Db 121 AAVRP--DLVAVSYVSGAPHR-----GSDTADFIROIIPGSGAGEAIVAGI----- 163

QY 178 KNAQIHGVGHI-----GLMNSQVNSL-IRKGLNGCG 208

Db 164 ----VNGIGALINFLSGSSSTSPONALCALLESINSEG 196

RESULT 12

US-08-232-519-2

; Sequence 2, Application US/08232519

; Patent No. 5484725

GENERAL INFORMATION:

APPLICANT: Kageyama, Bunji

APPLICANT: Nakae, Masanori

APPLICANT: Yaqui, Shigeo

TITLE OF INVENTION: NORBORANE TYPE ESTER HYDROLASE

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232,519

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 5-96286

FILING DATE: 22-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr, James F

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: SHGN-4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9000

TELEFAX: (212) 596-9090

TELEX: 14-8367

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 388 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-232-519-2

Query Match 8.0%; Score 87.5; DB 1; Length 388;

Best Local Similarity 23.1%; Pred. No. 0.3;

Matches 40; Conservative 34; Mismatches 60; Indels 39; Gaps 8;

QY 33 EHNPNVAVHGGIGASYNAGIKSYLVSG--WSRCKLYAVDFWMDKTGNNYNG---PVL 86

Db 134 EGTPIVLVHGFSG-----DISNMWLTODALAERRVIAFDLPGHGASSKNVGTGTLAFL 187

QY 87 SRFVQKVLDETGAKKVDIVAHSMGA-----NTPYIRKND-----GKNKIENVVTLG 134

Db 188 AGVYSELQTLKIEKAHVHSGGIALTLRHPDQVASINLAPGLGKDVADPIS 247

QY 135 GANSTSTKALPGDIPNCKILYTSYSSA-----DMIVNNYLSKLDGAKNA 180

Db 248 AFVSESSSRDM-----KAVLQMLVYNKALVGRKMWDAVLR--ARRLDGARD 292

RESULT 13

US-08-456-956-2

; Sequence 2, Application US/08456956

; Patent No. 5686285

GENERAL INFORMATION:

APPLICANT: Kageyama, Bunji

APPLICANT: Nakae, Masanori

APPLICANT: Yaqui, Shigeo

TITLE OF INVENTION: No. 5686285borane Type Ester Hydrolase

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/456,956

FILING DATE: 01-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 5-96286

FILING DATE: 22-APR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/232,519

FILING DATE: 22-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Haley Jr, James F

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: SHGN-4 DIV 1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

TELEX: 14-8367

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 388 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-456-956-2

Query Match 8.0%; Score 87.5; DB 1; Length 388;

Best Local Similarity 23.1%; Pred. No. 0.3;

Matches 40; Conservative 34; Mismatches 60; Indels 39; Gaps 8;

QY 33 EHNPNVAVHGGIGASYNAGIKSYLVSG--WSRCKLYAVDFWMDKTGNNYNG---PVL 86

Db 134 EGTPIVLVHGFSG-----DISNMWLTODALAERRVIAFDLPGHGASSKNVGTGTLAFL 187

QY 87 SRFVQKVLDETGAKKVDIVAHSMGA-----NTPYIRKND-----GKNKIENVVTLG 134

Db 188 AGVYSELQTLKIEKAHVHSGGIALTLRHPDQVASINLAPGLGKDVADPIS 247

QY 135 GANSTSTKALPGDIPNCKILYTSYSSA-----DMIVNNYLSKLDGAKNA 180

Db 248 AFVSESSSRDM-----KAVLQMLVYNKALVGRKMWDAVLR--ARRLDGARD 292

RESULT 14

US-09-134-001C-3517

; Sequence 3517, Application US/09134001C

; Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucelte-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US-60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3517
LENGTH: 652
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3517

Query Match

8.0%; Score 87; DB 4; Length 652;

Best Local Similarity 21.4%; Pred. No. 0.74;
Matches 47; Conservative 24; Mismatches 63; Indels 86; Gaps 11;

QY 26 QPSAKAEHN--PYVMVIGI-----GASVNFAGIKSYLVSGMSRGL 67
DB 26 QLTQAQYKNOYPVYFVHGFVGLVEDAFSMYPNMGKRYN---VKQELTLGTRVHA 316
QY 68 YAVDFMDTGTNYNNGPVLSRFQKVLDEFGA-----KRV 102
DB 317 NVGAF-----SSNYDRAVELYIKGRVDYGAHAHAKYGHKRYGRTYEGIMPDWEPGKKI 372
QY 103 DIVASHMGGAN--TPYIKN-----LDG--NKIENVVTIGANR 138
DB 373 HLVGSHMGGQTRLMHEHLRNGNDEIDYQRYGGTVSDLFKGGODNMVSTTLTLPN 432
QY 139 STSKALPGTDPNOKILYTSYSSADMIWNYLSKLDGAK 178
DB 433 GT-----PAAD---KLGSTKFIKD---TINRIGKIGTK 460

RESULT 15

US-09-111-556A-3

Sequence 3, Application US/09111556A

Patent No. 6020180

GENERAL INFORMATION:

APPLICANT: Svendsen, Allan

APPLICANT: Patnar, Shamkant A

APPLICANT: Egel-Mitani, Michi

APPLICANT: Borch, Kim

APPLICANT: Clausen, Ib G

APPLICANT: Hansen, Mogens T

TITLE OF INVENTION: C. ANTARCTICA LIPASE AND LIPASE VARIANTS

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6020180c No. 6020180disk of No. 6020180ch America, Inc.

STREET: 405 Lexington Avenue, 64th Floor

CITY: New York

STATE: New York

COUNTRY: United States of America

ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Tape

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/111,556A

FILING DATE: 22-DEC-1994

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DK PCT/DK93/00225

FILING DATE: 03-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Lambiris, Elias J.

REGISTRATION NUMBER: 33,728

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-867-0123

TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 277 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-111-556A-3

Query Match

8.0%; Score 86.5; DB 3; Length 277;

Best Local Similarity 26.4%; Pred. No. 0.23;
Matches 29; Conservative 21; Mismatches 49; Indels 11; Gaps 4;

QY 36 PYVMVHIGI-----GASVNFAGIKSYLVSGMSRGLAVDFMDTGTNYNNGPVLSRFV 90
DB 10 PILVHGLGFGFDRIGSHHYFHGKQALNECGAS---VFVPIISAANDSEARGDOLKQI 65
QY 91 QKVLDETGAKKVDIVASHMGGANFTPYIKNLDGKNKIENVVTIGANRST 140
DB 66 HMLRQVGAQRVNLIGHSO-GALTIARYAAT-APELIASVTSVSGPNHGS 113

Search completed: May 9, 2003, 16:22:45

Job time : 16 secs

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GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 16:22:01 ; Search time 20 Seconds
(without alignments)
975.473 Million cell updates/sec

Title: US-09-905-666a-55

Perfect score: 1088

Sequence: 1 MKFVKRRRIALVTILVLSVT.....NSQVSLIKELGNGGNTN 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 349150 seqs, 92025710 residues

Total number of hits satisfying chosen parameters: 349150

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PTCT_NEW_PUB pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/PCYUS_PUBCOMB pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1060	97.4	212	US-10-028-247-4	Sequence 4, Appl1
2	156	14.3	324	US-09-738-626-3593	Sequence 3593, Ap
3	130	11.9	300	US-09-738-626-3594	Sequence 3594, Ap
4	123	11.3	363	US-10-147-467-2	Sequence 2, Appl1
5	101.5	9.3	299	US-10-080-644-6	Sequence 6, Appl1
6	92.5	8.5	1062	US-09-815-242-5111	Sequence 5111, Ap
7	89.5	8.2	308	US-10-080-644-8	Sequence 8, Appl1
8	88	8.1	311	US-09-815-242-11886	Sequence 11886, A
9	87.5	8.0	464	US-09-912-020-281	Sequence 281, App
10	87	8.0	315	US-10-098-174-1	Sequence 1, Appl1
11	86.5	8.0	518	US-10-080-644-2	Sequence 2, Appl1
12	86.5	8.0	690	US-09-815-242-5841	Sequence 5841, Ap
13	85	7.8	262	US-10-027-805-35	Sequence 35, Appl1
14	85	7.8	262	US-10-027-804-35	Sequence 35, Appl1
15	85	7.8	262	US-09-903-410-35	Sequence 35, Appl1
16	85	7.8	1023	US-09-884-696-5	Sequence 5, Appl1
17	82.5	7.6	259	US-09-738-626-3604	Sequence 3604, Ap
18	80.5	7.4	379	US-09-813-408-12	Sequence 12, Appl1
19	80	7.4	350	US-10-108-605-65	Sequence 65, Appl1

20	79	7.3	235	US-09-533-029-74	Sequence 74, Appl1
21	79	7.3	836	US-09-858-525A-10	Sequence 10, Appl1
22	79	7.3	871	US-09-858-525A-2	Sequence 2, Appl1
23	79	7.3	1463	US-09-971-536-69	Sequence 69, Appl1
24	78	7.2	503	US-10-211-962-64	Sequence 64, Appl1
25	77.5	7.1	495	US-10-213-990-42	Sequence 42, Appl1
26	77.5	7.1	1093	US-09-801-368-4392	Sequence 392, App
27	76.5	7.0	254	US-10-080-644-5	Sequence 5, Appl1
28	76.5	7.0	372	US-09-813-408-9	Sequence 9, Appl1
29	76	7.0	275	US-08-322-678-8	Sequence 8, Appl1
30	76	7.0	275	US-09-813-408-18	Sequence 18, Appl1
31	76	7.0	275	US-10-033-325-4	Sequence 4, Appl1
32	76	7.0	275	US-09-060-854B-4	Sequence 4, Appl1
33	76	7.0	280	US-09-731-872-314	Sequence 14, App
34	76	7.0	357	US-09-837-235-15	Sequence 15, Appl1
35	76	7.0	434	US-09-971-536-62	Sequence 62, Appl1
36	75.5	6.9	380	US-09-813-408-16	Sequence 16, Appl1
37	75	6.9	297	US-10-080-644-7	Sequence 7, Appl1
38	75	6.9	535	US-09-995-749A-13	Sequence 13, Appl1
39	75	6.9	1781	US-09-995-749A-2	Sequence 2, Appl1
40	74.5	6.8	274	US-08-322-678-9	Sequence 9, Appl1
41	74.5	6.8	274	US-09-813-408-17	Sequence 17, Appl1
42	74.5	6.8	274	US-10-033-325-5	Sequence 5, Appl1
43	74.5	6.8	274	US-09-060-854B-5	Sequence 5, Appl1
44	74.5	6.8	363	US-09-797-464A-11	Sequence 11, Appl1
45	74	6.8	184	US-09-734-017A-78	Sequence 78, Appl1

ALIGNMENTS

RESULT 1
US-10-028-247-4
Sequence 4, Application US/10028247
Patent No. US20020150594A1
GENERAL INFORMATION:
APPLICANT: Goldman, Stanley
APPLICANT: Lathrop, Stephanie J.
APPLICANT: Longchamp, Pascal F.
APPLICANT: Whalen, Robert G.
TITLE OF INVENTION: Methods and Compositions for Developing Spore Display
FILE REFERENCE: 18097A-033520US
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US/10/028,247
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 60/214,161
PRIOR FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 212
TYPE: PRT
ORGANISM: Bacillus circulans
FEATURE:
OTHER INFORMATION: lipase 396
US-10-028-247-4
Query Match 97.4%; Score 1060; DB 12; Length 212;
Best Local Similarity 97.6%; Pred. No. 6.9e-97;
Matches 207; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 MKFVKRRRIALVTILVLSVSLFAMQPSAKAEHNPVYVHGIGASTNFGIKSYLSQ 60
DB 1 MKFVKRRRIALVTILVLSVSLFAMQPSAKAEHNPVYVHGIGASTNFGIKSYLSQ 60
QY 61 GMSRGKLYAVDFMDKTGTNNYNGPVLSREYQKVLDETGAKKVDIVAHSMGCAANTPYIKN 120
DB 61 GMSRGKLYAVDFMDKTGTNNYNGPVLSREYQKVLDETGAKKVDIVAHSMGCAANTLYIKN 120
QY 121 LDGKNKIENVVTLGAGNRSTTSKALPGTDPNOKILYTSYSSADMIYVNTLSKIDGAKNA 180

Db 121 LDGNGKLENNVTGGAGNRLTTSKALPCTDPNOKLLYTSIYSSADIMVWYLSKLDGAKNV 180
QY 181 QIHGVGHIGLMSQVNSLIKEGLNGGONTN 212
Db 181 QIHGVGHIGLMSQVNSLIKEGLNGGONTN 212

RESULT 2

US-09-738-626-3593
; Sequence 3593, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:

APPLICANT: MAKAGAMA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738, 626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 3593
LENGTH: 324
TYPE: PRT
ORGANISM: *Corynebacterium glutamicum*
US-09-738-626-3593

Query Match 14.3%; Score 156; DB 9; Length 324;
Best Local Similarity 32.7%; Pred. No. 1.9e-07;
Matches 35; Conservative 25; Mismatches 43; Indels 4; Gaps 2;

QY 36 PYVAVHIGGASYNFAGIKSYLVSGHSRCKLAVDFMDK-TGTYNNNGPVLSEFVQKVL 94
Db 91 PYVAVHIGGASYNFAGIKSYLVSGHSRCKLAVDFMDK-TGTYNNNGPVLSEFVQKVL 147
QY 95 DETGAKKVDIVAHSMGANTPYIKNLDGKNKIENTVTLGKANRST 141
Db 148 LATGASKVIVVGHSGGVLLRYMVRVLGASVKYKHMVSLAVPNHGT 194

RESULT 3

US-09-738-626-3594
; Sequence 3594, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:

APPLICANT: MAKAGAMA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738, 626
CURRENT FILING DATE: 2000-12-18

PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 3594
LENGTH: 300
TYPE: PRT
ORGANISM: *Corynebacterium glutamicum*
US-09-738-626-3594

Query Match 11.9%; Score 130; DB 9; Length 300;
Best Local Similarity 24.4%; Pred. No. 6.4e-05;
Matches 33; Conservative 33; Mismatches 47; Indels 22; Gaps 5;

QY 36 PYVAVHIGGASYNFAGIKSYLVSGHSRCKLAVDFMDKTYNNNGPY-----LSRF 89
Db 72 PYVAVHIGGASYNFAGIKSYLVSGHSRCKLAVDFMDKTYNNNGPY-----LSRF 123
QY 90 VOKVDETGAKKVDIVAHSMGANTPYIKNLDGKNKIENTVTLGKANRST-----T 141
Db 124 IDAVLVGTGAQIVLVGHSGGVVARYMRTYGGYKVRHMISITPNHGTLMGILNPM 183
QY 142 SKALPGTDPNOKILY 156
Db 184 TKVSGEGTIEKLHM 198

RESULT 4

US-10-147-467-2
; Sequence 2, Application US/10147467
; Publication No. US20030027295A1
; GENERAL INFORMATION:

APPLICANT: TAKESHI, Ishii
APPLICANT: SATOSHI, Mitsuda
TITLE OF INVENTION: ESTERASE GENE AND ITS USE
FILE REFERENCE: 20-4336P
CURRENT APPLICATION NUMBER: US/10/147,467
CURRENT FILING DATE: 2002-05-17
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 363
TYPE: PRT
ORGANISM: *Burkholderia cepacia*
US-10-147-467-2

Query Match 11.3%; Score 123; DB 9; Length 363;
Best Local Similarity 27.0%; Pred. No. 0.0004;
Matches 43; Conservative 27; Mismatches 59; Indels 30; Gaps 9;

QY 13 TIVLVSTSLFAPQPSAK-----AAEHPVAVVHIGGASYNFAGIKSYLVSGWSR--- 64
Db 26 TVLAMSLAGAQAASATTAVDYAATRYPIIVHGLGTG-KYGGVVEY-----WRIPE 79
QY 65 -----GKLYAVD---FMDKTYNNNGPVLSEFVQKVDGAKKVDIVAHSMGANTP 115
Db 80 DLRHGAAYVAVNLGSGFSDGPN-GRGEOLLAFFVKQVLAATGAOKVNLIGHSGGL-TS 137
QY 116 YIKNLDGKNKIENTVTLG-----KANRSTSKALPGTDP 150
Db 138 RYVASV-APELVASVTTISTPHWGSOPADPVOOLLQTPD 175

RESULT 5

US-10-080-644-6
; Sequence 6, Application US/10080644
; Patent No. US20020137172A1
; GENERAL INFORMATION:
APPLICANT: Glucksmann, Maria, Alexandra et al.

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Query Match      8.5%   Score 92.5; DB 10; Length 1062;
Best Local Similarity 25.3%; Pred. No. 1.8;
Matches 60; Conservative 22; Mismatches 78; Indels 77; Gaps 12;
```

RESULT 8
US-09-815-242-11886
Sequence 11886, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578

Db 122 DLQDLPLPOLGLVPCVYVGHSMG 144

RESULT 12

US-09-815-242-5841

; Sequence 5841, Application US/09815242

; Patent No. US20020061569A1

GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Karl L.

; APPLICANT: Zyskind, Judith W.

; APPLICANT: Wall, Daniel

; APPLICANT: Trivick, John D.

; APPLICANT: Carr, Grant J.

; APPLICANT: Yamamoto, Robert T.

; TITLE OF INVENTION: Identification of Essential Genes in

; FILE REFERENCE: ELITRA.011a

; CURRENT APPLICATION NUMBER: US/09/815,242

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5841

; LENGTH: 690

; TYPE: PR

; ORGANISM: Staphylococcus aureus

US-09-815-242-5841

Query Match

Best Local Similarity 24.1%; Score 86.5; DB 10; Length 690;

Matches 48; Conservative 23; Mismatches 55; Indels 73; Gaps 9;

QY 36 PVTMVGIGG-----AST-NEAIGKSYLV-----SQGMSRGKLYAVDFMDKTGTNNYN 82

Db 306 PVTMVGIGG-----AST-NEAIGKSYLV-----SQGMSRGKLYAVDFMDKTGTNNYN 82

QY 83 GPVLSFVGKVIDETGA-----KKVDIVAHSMGCAATPY 117

Db 362 AVELYIYIGRVYDAHAIAKYGHERYGTGKIPNMEPGKRVHLVGHSMGSGTIRLM 421

QY 118 IKNLGDNKIE-----NVVTLGGANR-----STTSKALP-----GTDPMQ 152

Db 422 EEFLLRNGNEELAYHKAHGEISPLFTGGHNNVVASITTLATPHNGSQADKFCNTEAAR 481

QY 153 KILYT-----STYSADM 165

Db 482 KIMFALNRFMGKNKYSIDL 500

RESULT 13

US-10-027-805-35

; Sequence 35, Application US/10027805

; Patent No. US20020164725A1

GENERAL INFORMATION:

; APPLICANT: ROBERTSON, Daniel E.

; APPLICANT: MURPHY, Dennis

; APPLICANT: REID, John

; APPLICANT: ROBERTSON, Daniel E.

; APPLICANT: MURPHY, Dennis

; APPLICANT: REID, John

; APPLICANT: ROBERTSON, Daniel E.

; APPLICANT: MURPHY, Dennis

; APPLICANT: REID, John

; APPLICANT: ROBERTSON, Daniel E.

; APPLICANT: MURPHY, Dennis

MAFFIA, Anthony

LINK, Steven

SWANSON, Ronald V.

WARREN, Patrick V.

KOSMOTKA, Anna

TITLE OF INVENTION: ESTERASES

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: FISH & RICHARDSON P.C.

STREET: 4225 EXECUTIVE SQUARE, STE 1400

CITY: LA JOLLA

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/027,805

FILING DATE: 21-Dec-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/602,359

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: HATLE, LISA A.

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 09010/010001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-678-5070

TELEFAX: 619-678-5099

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 262 AMINO ACIDS

TYPE: AMINO ACID

TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN

SEQUENCE DESCRIPTION: SEQ ID NO: 35:

US-10-027-805-35

Query Match

Best Local Similarity 7.8%; Score 85; DB 9; Length 262;

Matches 40; Conservative 23; Mismatches 62; Indels 34; Gaps 8;

QY 36 PVTMVGIGGASYNFAGISLYLSVQGMSRGKLYAVD-----FMDKTGTNNNGPV---LS 87

Db 22 PIVFVHG-WTANNF-----WKEDRRYFAGRNMMLFVDNRGHRSDKPLGYDFY 69

QY 88 RF-----VOKVDETGAKKVDIVAHSMGCAATPYIKNLGDNKIEENVVTLGGANRSTT 141

Db 70 RFENFTSDLDVAVREVEFEVYLVGHSPGIMSMKICS--EYNNRYLALLIIGGSRIRKL 127

QY 142 SKALPSTDPNOKILTYSTIYSSADMIVANLYLSKLDGAKNA 180

Db 128 LHR1--GYPLAKILIASIAVKKSSRLV-----ADLSFCKNA 160

RESULT 14

US-10-027-804-35

; Sequence 35, Application US/10027804

; Publication No. US20030054530A1

GENERAL INFORMATION:

; APPLICANT: ROBERTSON, Daniel E.

; APPLICANT: MURPHY, Dennis

; APPLICANT: REID, John

; APPLICANT: MAFFIA, Anthony

; APPLICANT: LINK, Steven

; APPLICANT: SWANSON, Ronald V.

; APPLICANT: WARREN, Patrick V.

; APPLICANT: KOSMOTKA, Anna

; APPLICANT: TITLE OF INVENTION: ESTERASES

NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
STREET: 4225 EXECUTIVE SQUARE, STE 1400
CITY: LA JOLLA
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/027,804
FILING DATE: 21-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,359
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: HAILE, LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 09010/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-10-027-804-35
Query Match 7.8%; Score 85; DB 9; Length 262;
Best Local Similarity 25.2%; Pred. No. 1.5;
Matches 40; Conservative 23; Mismatches 62; Indels 34; Gaps 8;
Qy 36 PVVAVHIGIGASYNFAGIKSYLVSGWSRGLAYD----FMDKTGTNNNGPY---LS 87
Db 22 PIVEFHG-WTANMNF-----WKEQRRYFAGRNMLFVDNRGHSRDKPLGYDFY 69
Qy 88 RF-----VQKVLDTGAKKVDIVAHSMGANTPIYIKNLDSGAKIENVVTLGGANRSTT 141
Db 70 RFENFISLDLDAVAVRETGVKEFVLGHSFGTMSMKYCS--EYRNRYLALILILIGGSRIKL 127
Qy 142 SKALPGTDPNOKIITYTSIYSSADMIVMNYLSKLDGAKNA 180
Db 128 LHRI--GYPLAKILASIAVKKSSRLV----ADLSFGKNA 160
RESULT 15
US-09-903-410-35
Sequence 35, Application US/09903410
Patent No. US20020146799A1
GENERAL INFORMATION:
APPLICANT: DIVERSA CORPORATION
APPLICANT: ROBERTSON, Dan
APPLICANT: MURPHY, Dennis
APPLICANT: REID, John
APPLICANT: MAFFIA, Anthony
APPLICANT: LINK, Steven
APPLICANT: SWANSON, Ronald
APPLICANT: WARREN, Patrick
APPLICANT: KOSMOTKA, Anna
TITLE OF INVENTION: ENZYMES HAVING ESTERASE ACTIVITY AND METHODS OF USE THEREOF
FILE REFERENCE: DIVER180-2
CURRENT APPLICATION NUMBER: US/09/903,410
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 09/382,242
PRIOR FILING DATE: 1999-08-24

PRIOR APPLICATION NUMBER: US 08/602,359
PRIOR FILING DATE: 1996-02-16
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.0
SEQ ID NO 35
LENGTH: 262
TYPE: PRT
ORGANISM: Archaeoglobus Veneficus
US-09-903-410-35
Query Match 7.8%; Score 85; DB 10; Length 262;
Best Local Similarity 25.2%; Pred. No. 1.5;
Matches 40; Conservative 23; Mismatches 62; Indels 34; Gaps 8;
Qy 36 PVVAVHIGIGASYNFAGIKSYLVSGWSRGLAYD----FMDKTGTNNNGPY---LS 87
Db 22 PIVEFHG-WTANMNF-----WKEQRRYFAGRNMLFVDNRGHSRDKPLGYDFY 69
Qy 88 RF-----VQKVLDTGAKKVDIVAHSMGANTPIYIKNLDSGAKIENVVTLGGANRSTT 141
Db 70 RFENFISLDLDAVAVRETGVKEFVLGHSFGTMSMKYCS--EYRNRYLALILILIGGSRIKL 127
Qy 142 SKALPGTDPNOKIITYTSIYSSADMIVMNYLSKLDGAKNA 180
Db 128 LHRI--GYPLAKILASIAVKKSSRLV----ADLSFGKNA 160
Search completed: May 9, 2003, 16:29:38
Job time : 22 secs

GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 16:19:36 ; Search time 20 Seconds
(without alignments)
1019.025 Million cell updates/sec

Title: US-09-905-666a-55

Perfect score: 1088

Sequence: 1 MKFVKRRITIALVTLLVLSVT.....NSQVNSLJKEGINGGQNTN 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

283224

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1020	93.8	212	2	S23934
2	731.5	67.2	210	2	C69652
3	208	19.1	237	2	G75316
4	178	16.4	290	2	T36757
5	153.5	14.1	202	2	S77556
6	149	13.7	286	2	T26657
7	145	13.3	211	2	AE1975
8	142.5	13.1	344	2	T27932
9	139.5	12.8	300	2	T20712
10	139.5	12.8	358	1	AA8952
11	137.5	12.6	371	2	T28853
12	131.5	12.1	474	2	B69470
13	131	12.0	292	2	T33322
14	130	11.9	364	1	A39133
15	130	11.9	479	2	A97027
16	129	11.9	300	2	AD1551
17	124.5	11.4	171	2	S15911
18	124.5	11.4	339	2	C82486
19	123.5	11.4	329	2	T24285
20	122	11.2	364	1	JT0579
21	121	11.1	323	2	S61927
22	121	11.1	333	2	T22227
23	119	10.9	340	2	T31812
24	115.5	10.6	335	2	T18906
25	115	10.6	309	2	G83044
26	111	10.2	488	2	A95301
27	109	10.0	281	2	T20894
28	107	9.8	277	2	T32460
29	106	9.7	497	2	H83886

30	104.5	9.6	299	2	AF1193	hypothetical prote
31	103.5	9.5	237	2	T26660	hypothetical prote
32	101.5	9.3	299	2	T23932	hypothetical prote
33	100.5	9.2	681	2	G90075	triacylglycerol 11
34	97.5	9.0	268	2	S73694	triacylglycerol 11
35	97.5	9.0	1519	2	S41525	major ring-forming
36	96.5	8.9	1335	2	T17508	glycoprotein Vp260
37	96	8.8	377	2	AB2713	triacylglycerol 11
38	94.5	8.7	438	2	B83295	hypothetical prote
39	94	8.6	267	2	F90516	esterase/lipase 1
40	94	8.6	688	2	AA7705	triacylglycerol 11
41	93.5	8.6	272	2	E97008	periplasmic amino
42	93.5	8.6	638	2	AA0340	putative autotransp
43	93	8.5	682	2	S68970	triacylglycerol 11
44	92.5	8.5	1062	2	F83335	RND multidrug effl
45	92.5	8.5	1062	2	T30830	hypothetical prote

ALIGNMENTS

Result 1

S23934

Lipase lipA - Bacillus subtilis

C:Species: Bacillus subtilis

C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 15-Oct-1999

C:Accession: S23934; B69652

R:Darais, V., Baulard, A., Schanck, K., Colson, C.

Biochim. Biophys. Acta 131, 253-260, 1992

A:Title: Cloning, nucleotide sequence and expression in Escherichia coli of a lipase

A:Reference number: S23934; MUID:92329538; PMID:1320940

A:Accession: S23934

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-212 <DAR>

A:Cross-references: GB:M74010; MID:9143153; PIDN:AAA2574.1; PID:9143154

R:Kunst, F., Ogasawara, N., Moser, I., Albertini, A.M., Alloni, G., Azevedo, V., Ber

C:Bron, S., Brouillet, S., Brusch, C.V., Caldwell, B., Capiano, V., Carter, N.M.,

A:Enllich, S.D., Emerson, P.T., Entlan, K.D., Errington, J., Fabret, C., Ferrati,

Nature 390, 249-256, 1997

A:Authors: Foulger, C.D., Fritz, C., Fujita, M., Fujita, Y., Fuma, S., Galizzi, A., Gal

lech, J., Harwood, C.R., Henaut, A., Hilbert, H., Holsappel, S., Hosono, S., Hullo, M

Koelter, P., Konigstein, G., Krogh, S., Kumano, M., Kurita, K., Lapidus, A., Lardio

A:Authors: Lauber, J., Lazarevic, V., Lee, S.M., Levine, A., Liu, H., Masuda, S., Mau

Y, M., Ogawa, K., Ogiwara, A., Oudega, B., Park, S.H., Parro, V., Pohl, T.M., Portete

Rieger, M., Rivolta, C., Rocha, E., Roche, B., Rose, M., Sadate, Y., Sato, T., Scani

A:Authors: Schleich, S., Schroeter, R., Scifione, F., Sekiguchi, J., Sekowska, A., Se

akeuchi, M., Tamakoshi, A., Tanaka, T., Terpstra, P., Togonoh, A., Tosato, V., Uchida

T., Winters, P., Wipat, A., Yamamoto, H., Yamane, K., Yasumoto, K., Yata, K., Yoshida

A:Authors: Yoshikawa, H.F., Zumbstein, E., Yoshikawa, H., Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis

A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: B69652

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-132, 'L', 134-212 <RUN>

A:Cross-references: GB:Z99105; GB:AL009126; MID:92632457; PIDN:CAB12064.1; PID:el1822

A:Experimental source: strain 168

C:Genetics:

A:Gene: lipA

Query Match

Best local similarity 92.9%; Score 1020; DB 2; Length 212;

Matches 197; Conservative 8; Mismatches 7; Indels 0; Gaps 0.

QY 1 MKFVKRRITIALVTLLVLSVTSLPAMQPSAKAAEHNPVWVHGIGASVYFAGIKSYLSQ 60

DB 1 MKFVKRRITIALVTLLVLSVTSLPALQPSAKAAEHNPVWVHGIGASVYFAGIKSYLSQ 60

QY 61 GMSRGLVAVDFMDKGTGTNYNGPVLSRPFVCKVLDLGTGKKYDIYVHSGNGANTPYTKN 120

DB 61 GMSRGLVAVDFMDKGTGTNYNGPVLSRPFVCKVLDLGTGKKYDIYVHSGNGANTPYTKN 120

C:Species: *Synechocystis* sp.

A:Variate: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

C:Accession: S77556

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M. Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S77556

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-202 <KAN>

A:Cross-references: EMBL:D90905; GB:AB001339; NID:g152360; PIDN:BA17403.1; PID:d101813

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Genetics:

A:Start codon: GTG

Query Match

Best Local Similarity 14.1%; Score 153.5; DB 2; Length 202;

Matches 35; Conservative 27; Mismatches 45; Indels 7; Gaps 3;

OY 29 AKAAENPVVHVGIGASYNFAGIKSYLVSGMSRGKLYAVDFMDKTGTNNNGPYLSR 88

DB 3 AEPDRHPPVLYIGIYDTRAKFATWDFLTKGMS--VHCLDLVPNDGS--TSLALLAE 57

OY 89 FVOKVLDERGA--KQVDIVAHSMGANTPYIKNLGDKNKIENVVTLGGANRST 140

DB 58 QAKYIDOKFAPQDPVLDIGFSMGLVTRYIQLRGGERVRRYITISAPNOGT 111

RESULT 6

hypothetical protein Y38E10A.g - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C:Accession: T26557

R:Wallis, J.

A:Reference number: Z20252

A:Accession: T26557

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-286 <WILD>

A:Cross-references: EMBL:AL110484; PIDN:CA854398.1; CESP:Y38E10A.g

A:Experimental source: clone Y38E10A

C:Genetics:

A:Gene: CESP:Y38E10A.g

A:Introns: 63/2; 221/2; 261/3

C:Superfamily: *Caenorhabditis elegans* hypothetical protein C09E8.2

Query Match

Best Local Similarity 13.7%; Score 149; DB 2; Length 286;

Matches 55; Conservative 30; Mismatches 71; Indels 55; Gaps 8;

OY 36 PVMVHVGIGASYNFAGIKSYLVSGMSRGKLYAVDFMDKTGTNNNGPYLSRFOVKV-- 93

DB 66 PVLVHGTNSAGTFAPQAAVFRANCMSEETVATITGACGVTATNNVKKLCERYQDIRN 125

OY 94 ----LDEFGAKVDIVAHSMGANTPYIKNLGDKNKIENVVTLG-----G 135

DB 126 MILAVNAFTQOKVNVIGYSMG--SPIARKAILGGCAEYVQLGAPLFTSIETIYSVAG 182

OY 136 ANRST-----TSKALPG-----TDPNOKILY-----SISSAD----- 164

DB 183 ANNGTLCIDILRAPLVPPCNTKNGKSCSDFLTDIRSVSAVEGQYIFSTIGPSDKVGF 242

OY 165 MIWNYLSKLDGAKNAQIHGVG--HIGLLMNS 194

DB 243 NFVCGVRSRIDGATAEKDNVPGNHDAIANT 273

RESULT 7

AE1975

hypothetical protein alr1352 [imported] - *Nostoc* sp. (strain PCC 7120)

C:Species: *Nostoc* sp.

A:Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002

C:Accession: AE1975

R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kunitz, T.; Sasamoto, S.; Watanabe, A.; Irtigu

Nakazaki, M.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AE1975

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-211 <KUR>

A:Cross-references: GB:BA000019; PIDN:BA873309.1; PID:g17130699; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: alr1352

Query Match

Best Local Similarity 13.3%; Score 145; DB 2; Length 211;

Matches 54; Conservative 33; Mismatches 77; Indels 40; Gaps 8;

OY 33 EHNPPVHVGIGASYNFAGIKSYLVSGMSRGKLYAVDFMDKTGTNNNGPYLSRFVQ 91

DB 7 QRRPVLYHGHITTEVFENPMAYLRQLGHTVTLVLP-----NNGEAPLVNLAQ 57

OY 92 KVLDE-----TGAKKVDIVAHSMGANTPYIKNLGDKNKIENVVTLGGANRST--SK 143

DB 58 QVADVYCATITTPQPPDVLGFSMGIVSRYYQKLGISRGVQFVITSSPHGTVAAVYS 117

OY 144 ALPG-----TDPN-----OKILYTSISSAD--MIWNYLSKLDGAKNAQIHGV 185

DB 118 QHPCGVQMRNSLFLDLNNDVQMLEOLNFTSIWTFYDLMIITPHSSKMPVGEKELPIVA 177

OY 186 GHIGLLMN-----SOVNSLKEGLN 205

DB 178 LHSMLKDRPSTRAVAALAEPIIN 201

RESULT 8

T27932

hypothetical protein ZK617.2 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T27932

R:White, S.

A:Reference number: Z20442

A:Accession: T27932

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-344 <WILD>

A:Cross-references: EMBL:Z73897; PIDN:CA98062.1; GSPDB:GN00022; CESP:ZK617.2

A:Experimental source: clone ZK617

C:Genetics:

A:Gene: CESP:ZK617.2

A:Introns: 62/2; 121/3; 288/2

Query Match

Best Local Similarity 13.1%; Score 142.5; DB 2; Length 344;

Matches 53; Conservative 29; Mismatches 65; Indels 57; Gaps 9;

OY 36 PVMVHVGIGASYNFAGIKSYLVSGMSRGKLYAVDFMDKTGTNNNGPYLS----- 87

DB 65 PVEFVHGLNNEAGSLWKIARDFTNANYPROYLFAT--WGKGFPLMLNVAMSCTHVQHYR 123

OY 88 RFVQKVLDEFGAKKVDIVAHSMGANTPYIKNLGDKNKIEN-----VVT 132

DB 124 RFLETVLKYTGAKQIDVIGYSMG--SPIARKAILGGKCVADNPVVALGPSLHSRVHTYIS 180

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Oy    133 LCGANSTSKLPL-----GTDPNOKIL-----TYSIY-----SSALMIWN   169
      |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db    181 VAGANGSOLCALPPFDICNMKTGLMCNSKFLIEDINMFNKGSTAKFNLASTADPVV-G   239
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy    170 YL-----SKLDGNKNAQIHGVGH   187
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db    240 YMACKKASEFTGAHEMKVEGRNH   263
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 9
T20712
hypothetical protein F10P2.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C:Accession: T20712
R:Coles, L.
submitted to the EMBL Data Library, August 1994
A:Reference number: Z19313
A:Accession: T20712
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-300 <WILL>
A:Cross-references: EMBL:Z35598; PIDs:CAA84650.1; GSPDB:GND0021; CESP:F10P2.3
A:Experimental source: clone F10P2
C:Genetics:
A:Gene: CESP:F10P2.3
A:Map position: 3
A:introns: 13/2; 115/2; 208/3; 268/1
C:Superfamily: Caenorhabditis elegans hypothetical protein C09E8.2

Query Match          12.8%; Score 139.5; DB 2; Length 300;
Best Local Similarity 31.4%; Pred. No. 0.00037;
Matches 43; Conservative 17; Mismatches 50; Indels 27; Gaps 5;

Oy    28 SAKAAEHNPVNVWHIGICASY-----NFAGIKSYLVSGMGRKLYAVDFMDKTGT-   78
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db    36 SDDPYEKPEVPIRHSGDTALTFOOPLATGFERSIOYELEQMYTEAEIYATTWGDTSVG   95
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Oy    79 -----NNNGVSVRSFPYKVLDETGAKKVDIVASMGANTPYRIKKLDGSKI-   127
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db    96 SMLDYYSTHTTCGNLLTYLRFLFENAVIGTGAKKVDIIAHSVG---VPLMRKYVKGGTLIG   152
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Oy    128 ENVTLTG---GANRST   140
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db    153 TDGNCITLGPPLCAKVDY   169
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 10
A48952
triacylglycerol lipase (EC 3.1.1.3) precursor - Pseudomonas glumae
C:Species: Pseudomonas glumae
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A48952; S36248; S37291
R:Fienken, L.G.; Edmond, M.R.; Batenburg, A.M.; Bos, J.W.; Visser, C.; Verrips, C.T.
Appl. Environ. Microbiol. 58: 3787-3791, 1992
A>Title: Cloning of the pseudomonas glumae lipase gene and determination of the active site
A:Reference number: A48952; MUID:931119130; PMID:1476423
A:Accession: A48952
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-358 <FR2>
A:Cross-references: EMBL:X70354; NID:g49205; PIDN:CAA49812.1; PID:g49206
A:Experimental source: pGI
A>Note: sequence extracted from NCBI backbone (NCBIT:121572, NCBI:P:121573)
R:Fienken, L.G.J.; Bos, J.W.; Visser, C.; Mueller, W.; Tommassen, J.; Verrips, C.T.
Mol. Microbiol. 9, 579-589, 1993
A>Title: An accessory gene, lipg, required for the production of active Pseudomonas glum
A:Reference number: S36248; MUID:94018652; PMID:8412704
A:Accession: S36248
A:Molecule type: DNA
A:Residues: 316-358 <FR2>
A:Cross-references: EMBL:X70354
```

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C:Genetics:
A:Gene: LipA
C:Superfamily: Pseudomonas triacylglycerol lipase
C:Keywords: carboxylic ester hydrolase, extracellular protein

Query Match          12.8%; Score 139.5; DB 1; Length 358;
Best Local Similarity 29.6%; Pred. No. 0.00046;
Matches 48; Conservative 26; Mismatches 59; Indels 29; Gaps 8;

OY 1 MKFVRRRLIALVTILVTSLSL-----FAMQPSAKAAE-----HNPVVVWHGIGGASY 48
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 2 VRSMRSVAARAVAMALVMPDLAGAGITMAAPAAVAADYATFRPVILVHDLGTD- 60
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

OY 49 NFA-----GIKSYLVSOQWSRGKLYAVD--FMDKTGTNYNNGPVLSPFQKVLDETG 98
      |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 61 KFAVAVDVWYGIGQSLQSHG---AKVYVANSIGSGSDGPN-GSGEQLAVVKQVLATG 116
      |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

OY 99 AKKVDIVAHSMGANTPYIYNLDGKNKIEVYVLGGANRST 140
      ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 117 ATKVNLIGHSGGLTSRYVA--AVAPOLVASVTITGPHRGS 156
      ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 11
T24853
hypothetical protein T12A7.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T24853
R:Lennard, N.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19943
A:Accession: T24853
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-371 <MIL>
A:Cross-references: EMBL:Z73911; PIDs:CAA98139.1; GSPDB:GNO0022; CESP:T12A7.4
A:Experimental source: clone T12A7
C:Genetics:
A:Gene: CESP:T12A7.4
A:Map position: 4
A:Introns: 105/3; 138/3; 166/2; 218/1; 261/3; 318/1; 343/3

Query Match          12.6%; Score 137.5; DB 2; Length 371;
Best Local Similarity 30.4%; Pred. No. 0.00071;
Matches 41; Conservative 22; Mismatches 35; Indels 37; Gaps 7;

OY 35 NPVVVWHGIGA-----SYNFAIGIKSYLVSOQWSRGKLYAVDFWDKTGt-----NYN 81
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 111 DPVIFEFHNSDALLTANNFSTGWTTVQYFLNCGYTLGLYGTG-WGNTNTTAAVERDHD 169
      |||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

OY 82 NGPV--LSRFQKVLDEFGARKKVDIVAHSMG-----GANPPYIKKNDG----- 123
      ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 170 CVYFRLKRFEVAVADYTGAKQKINLISHSMGVTLARKVYILG----YIMADGSCNIGKP 225
      ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

OY 124 -GNKIEVYVLGGAN 137
      ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 226 LGNKVAVILGIAGAN 240
      ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 12
B69470
lipase homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Jun-2000
C:Accession: B69470
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
.; Glöck, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Overbeek, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C.
.:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
.:Reference number: A69250; MUID:98049343; PMID:9389475

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Query Match	12.0%;	Score 131;	DB 2;	Length 292;
Best Local Similarity	24.1%;	Pred. No. 0.0018;		
Matches	40;	Conservative	32;	Mismatches 67; Indels 46; Gaps 6;
QY	17	LSVTSLEFAMOPSAKAEEHNPVVMVHIGIGASYNENAGISKYLVSGSGSKGIYAVDFWDKT	76	
		: : : : : : : : : : : : : : : : : : : : : : : : :		
Db	46	LGMASFEFGCKENPEVEPNPVIIVHIGITNNKASREGGTVAFLSKSGYKNSIEIGYGTWCDSG	105	
QY	77	GTYNNNGVYLSRFQKV-----LDETAKKVDIYAHSMGCGANTPYIYIKNDGKKIEV	130	
		: : : : : : : : : : : : : : : : : : : : : : : : :		
Db	106	RTPYGLVDMCKNVYKQIIRAMITIAVRQYTGQKVDYIGVSMG---SPLARKAILIGGCQVPT	162	
QY	131	VTLDG-----GANRSTTSKALP--GP-----DPNOKILYT	157	
		: : : : : : : : : : : : : : : : : : : : : : : : :		
Db	163	ELIAGPLTELVDYFLSVAGANGYGVLCILPPYVPGTCNNKNGLHCDSEFLQDINNHRTREG	222	
QY	158	-----SIYSAD	164	
		: : : : : : : : : : : : : : : : : : : : : : : : :		
Db	223	SHVESIESTAD	233	

QY 1 MKFKRRRLALVTLTVSYSLSPFMOSAKA-----EHN-----P 36
 166 LNIKRRFLVGYCC-IPINIEFMALYACHTAKLEIYDHDLKYITNKERDPSHCCKRYP 223
 QY 37 VVNHGIGGAS--YNNAG-IKSLVYSGQSRCGLY--ADEFMDKTGTNNNGPVLSEFV 90
 224 LVLVHGGRFLDKLYINWGRIPKELING--ATTIYGQDAW--GTVEYNQMYNNKI 277
 Db
 QY 91 QKVLDETGAKVDIVAHSMGCAATPYIKNLDGNGKIENVTLTGANRSTTKALPGTDP 150
 278 LQILKEGCEKVVNIASHSGDLSRYVASKIEMKRYAASLTMMSSPPRGCKPVDIACKIP 337
 Db

Mon May 19 10:47:10 2003

us-09-905-666a-55.rpr

Page 6

```

OY      151 NOKILYTSIYSSADMIYVNLKLDGAKNAQIHGVC-HIGLNNQVNSLIKE 202
      ::  || : | : | | : :| : | :
Db      338 DK-----IYRAVSNFFDKYY-KILGDKNPDEFYTASRQFSTYSSSKFNEEYVK 383

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Search completed: May 9, 2003, 16:22:24
Job time : 23 secs
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GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 16:17:45 ; Search time 12 Seconds
(Without alignments)
732.748 Million cell updates/sec

Title: US-09-905-666a-55

Perfect score: 1088
Sequence: 1 MKFVKRRRIALVTIIVLSVT.....NSQVNSLKEGLNGGCONTN 212

Scoring table:

BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1023	94.0	212	1 LIP_BACSU
2	139.5	12.8	358	1 LIP_PSEGL
3	125	11.5	364	1 LIP_BURCE
4	124.5	11.4	312	1 LIP_VIRCH
5	122	11.2	364	1 LIP_PSESS
6	97.5	9.0	268	1 ESI2_MYCPN
7	94	8.6	688	1 LIP_STAPB
8	88.5	8.1	373	1 ACOC_ALCEU
9	88	8.1	311	1 LIP_PSEAB
10	88	8.1	311	1 LIP_PSEAB
11	87.5	8.0	415	1 YEGM_ECOLI
12	87.5	8.0	1045	1 Y045_MYCPN
13	87	8.0	1953	1 BN11_YEAST
14	86.5	8.0	277	1 LIP_PSEER
15	86.5	8.0	293	1 MHPQ_ECOLI
16	86.5	8.0	690	1 LIP_STAAU
17	86	7.9	719	1 C1IA_BACTK
18	85	7.8	719	1 C1ID_BACTU
19	85	7.8	1023	1 HXY1_ECOLI
20	85	7.8	1052	1 R732_ACTPL
21	84	7.7	619	1 CHIT_STRII
22	83.5	7.7	213	1 XNNA_BACCI
23	83.5	7.7	456	1 ENO_MYCPV
24	83	7.6	501	1 TACY_PAEAL
25	82.5	7.6	268	1 ESI2_MYCCE
26	82	7.5	358	1 ALF_BUCAL
27	82	7.5	671	1 ALYS_ENTFA
28	82	7.5	1286	1 AIDA_ECOLI
29	81.5	7.5	213	1 XNNA_BACSU
30	81.5	7.5	351	1 ADH_CLOBE
31	81.5	7.5	623	1 PDAT_SCHPO
32	81	7.4	326	1 TGL2_YEAST
33	81	7.4	372	1 FLGI_BUCAT

34	81	7.4	662	1 YME1_SCHMA	P46508 schistosoma
35	81	7.4	684	1 FLID_HELPJ	Q92121 helicobacte
36	80	7.4	288	1 PIP_BACCO	P46541 bacillus co
37	80	7.4	350	1 GALE_DROME	O9W055 drosophila
38	80	7.4	381	1 SUBN_BACNA	P35835 bacillus su
39	80	7.4	427	1 TOLB_HAELN	P44677 haemophilus
40	80	7.4	587	1 YS48_CAEBL	Q09374 caenorhabdi
41	80	7.4	684	1 FLID_HELPY	P96786 helicobacte
42	79.5	7.3	274	1 SUBD_BACLI	P00781 bacillus li
43	79.5	7.3	288	1 Y134_MYCTU	O50599 mycobacteri
44	79	7.3	514	1 TUBE_DROVI	Q08171 drosophila
45	79	7.3	546	1 AMYB_BACCE	P36924 bacillus ce

ALIGNMENTS

RESULT 1

ID	LIP_BACSU	STANDARD	PRT	212 AA.
AC	P37957: 034644:			
DT	01-OCT-1994 (Rel. 30, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Lipase precursor (EC 3.1.1.3) (Triacylglycerol lipase).			
DE	LIPASE OR LIP.			
OS	Bacillus subtilis.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1423;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=168;			
RX	MEDLINE=92329538; PubMed=1320940;			
RA	Dattois V., Baulard A., Schanck K., Colson C.;			
RT	"Cloning, nucleotide sequence and expression in Escherichia coli of a			
RT	lipase gene from Bacillus subtilis 168."			
RT	Biochim. Biophys. Acta 1131:253-260(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=168;			
RA	Kunano M., Tamakoshi A., Yamane K.;			
RT	"A 32 kb nucleotide sequence from the region of the lincomycin-			
RT	resistance gene (22-25 degree) of the Bacillus subtilis chromosome and			
RT	identification of the site of the lin-2 mutation."			
RT	Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=168;			
RX	MEDLINE=98044033; PubMed=9384377;			
RA	Azevedo V., Bertero M.G., Bessieres P., Bojotin A., Borchert S.;			
RA	Borriess R., Boursier L., Brans A., Braun M., Brigelli S.C., Bron S.;			
RA	Boullier S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.;			
RA	Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.;			
RA	Dentzot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.;			
RA	Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.;			
RA	Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.;			
RA	Ghim S.Y., Glaser P., Goffeau A., Golligly E.J., Grandi G.;			
RA	Guiseppi G., Guy B.J., Haga K., Haehn J., Harwood C.R., Henaut A.;			
RA	Hilbert H., Holstappel S., Hosono S., Hullio M.F., Itaya M., Jones L.;			
RA	Joris B., Karamella D., Kasahara Y., Klerit Blanchard M., Klein C.;			
RA	Kobayashi Y., Koeltter P., Koningsstein G., Krogh S., Kumano M.;			
RA	Kunita K., Lapidus A., Lardinis S., Lauber J., Lazarevic V.;			
RA	Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C.;			
RA	Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.;			
RA	Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.;			
RA	Paro V., Pohl T.M., Portetelle D., Portoullik S., Prescott A.M.;			
RA	Pressecen E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.;			
RA	Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.;			
RA	Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.;			
RA	Selinguich J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.;			
RA	Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.;			
RA	Takeuchi M., Tamakoshi A., Tanaka T., Terpiltra P., Tognoni A.;			

RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viaril A., Wambuit R., Wedler E., Wedler H., Weitzengger T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danphin A.;
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*
 RT *subtilis*,"
 RL Nature 390:249-256(1997).
 CC -1- CATALYTIC ACTIVITY: triacylglycerol + H(2)O = diacylglycerol + a
 CC fatty acid anion.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -----
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 CC -----
 CC EMBL: W74010; AAA22574.1; -
 CC DR EMBL: AB000617; BAA22231.1; -
 CC DR EMBL: Z59105; CAB12064.1; -
 CC DR PIR: S23934; S23934.
 CC DR Subtilisin; BG10679; 1lpa.
 CC DR InterPro: IPR002918; Lipase_2.
 CC DR InterPro: IPR000379; Ser_estrs.site.
 CC DR Pfam: PF01674; Lipase_2; 1.
 CC DR Hydrolyase; Lipid degradation; Signal; Complete proteome.
 CC FT SIGNAL. 1 24
 CC FT CHAIN 25 212 LIPASE.
 CC FT ACT_SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT CONFLICT 133 133 L -> V (IN REF. 1).
 CC FT SEQUENCE 212 AA; 22791 MW; B6A70E02746118BF CRC64;
 CC -----
 CC Query Match 94.0%; Score 1023; DB 1; Length 212;
 CC Best Local Similarity 93.4%; Pred. No. 4.1e-79;
 CC Matches 198; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
 CC -----
 CC QY 1 MKRYKRIILVLTIVSVSLFMPQSAKAENPVYVWVHGICGASTYRAGISYLSQ 60
 CC DB 1 MKFYKRIILVLTIVSVSLFMPQSAKAENPVYVWVHGICGASTYRAGISYLSQ 60
 CC QY 61 GWSGKRYADEVMDKCTNNNGPVLSPFOKVDGAKKVDIVASMGANPYITKN 120
 CC DB 61 GWSGKRYADEVMDKCTNNNGPVLSPFOKVDGAKKVDIVASMGANPYITKN 120
 CC QY 121 LDGSKRIENVVTLGGANRSTTSKALPCTDPNOKILYTSIYSSADMIYVNLTKLDGAKNA 180
 CC DB 121 LDGSKRIENVVTLGGANRSTTSKALPCTDPNOKILYTSIYSSADMIYVNLTKLDGAKNA 180
 CC QY 181 QIHGVGHIGILMNSQVNSLIKEGNGGQNTN 212
 CC DB 181 QIHGVGHIGILMNSQVNSLIKEGNGGQNTN 212
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 CC RESULT 2
 CC LIP_PSEGL STANDARD: PRT; 358 AA.
 CC ID LIP_PSEGL
 CC AC 005489;
 CC DT 01-OCT-1994 (Rel. 30, Created)
 CC DT 01-OCT-1994 (Rel. 30, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE Lipase precursor (EC 3.1.1.3) (triacylglycerol lipase).
 CC GN LIPA.
 CC OS Pseudomonas glumae, and
 CC OS Chromobacterium viscosum.
 CC OC Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
 CC OC Burkholderia.
 CC NCBI_TaxID=337, 42739;
 CC RX [1]
 CC RC SEQUENCE FROM N.A., SEQUENCE OF 40-61, AND MUTAGENESIS.
 CC RP SPECIES=P. glumae; STRAIN=PGL / CBS 322.89;
 CC RX MEDLINE=93119130; PubMed=1476423;

RA Frenken L.G.J., Egmond M.R., Batenburg A.M., Bos J.W., Visser C.,
 RA Varrup C.T.;
 RT Cloning of the *Pseudomonas glumae* lipase gene and determination of
 RT the active site residues.";
 RL Appl. Environ. Microbiol. 58:3787-3791(1992).
 CC [2]
 CC SEQUENCE OF 40-54, AND CHARACTERIZATION.
 CC SPECIES=C. viscosum;
 CC RX MEDLINE=95306500; PubMed=7786905;
 CC RA Taipa M.A., Liberton K., Costa J.V., Cabral J.M.S., Jaeger K.E.;
 RT "Lipase from *Chromobacterium viscosum*: biochemical characterization
 RT indicating homology to the lipase from *Pseudomonas glumae*.";
 RL Biochim. Biophys. Acta 1256:396-402(1995).
 CC [3]
 CC X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 CC SPECIES=P. glumae;
 CC RX MEDLINE=94009622; PubMed=8405390;
 CC RA Noble M.E.M., Cleasby A., Johnson L.N., Egmond M.R., Frenken L.G.J.;
 RT "The crystal structure of triacylglycerol lipase from *Pseudomonas*
 RT *glumae* reveals a partially redundant catalytic aspartate.";
 RL FEBS Lett. 331:123-128(1993).
 CC [4]
 CC X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 CC SPECIES=C. viscosum; STRAIN=ATCC 6918;
 CC RX MEDLINE=96275636; PubMed=8683577;
 CC RA Lang D., Hoffmann B., Haalck L., Hecht H.-J., Spener F., Schmid R.D.,
 RA Schomburg D.;
 RT "Crystal structure of a bacterial lipase from *Chromobacterium*
 RT *viscosum* ATCC 6918 refined at 1.6-A resolution.";
 RL J. Mol. Biol. 259:704-717(1996).
 CC -1- FUNCTION: HYDROLYSIS OF TRIGLYCERIDES.
 CC -1- CATALYTIC ACTIVITY: triacylglycerol + H(2)O = diacylglycerol + a
 CC fatty acid anion.
 CC -1- COFACTOR: REQUIRES CALCIUM.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE AB HYDROLASE SUPERFAMILY. PSEUDOMONAS
 CC LIPASE FAMILY.
 CC -1- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
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 CC -----
 CC EMBL: X70354; CAA49812.1; -
 CC DR EMBL: A16323; CAA01279.1; -
 CC DR EMBL: A32021; CAA02073.1; -
 CC DR PIR: A48952; A48952.
 CC DR PIR: S37291; S37291.
 CC DR PDB: 1TAH; 3I-MAY-94.
 CC DR InterPro: IPR000073; Abhydrolase.
 CC DR InterPro: IPR000734; Lipase.
 CC DR InterPro: IPR000379; Ser_estrs.site.
 CC DR Pfam: PF00561; abhydrolase_1.
 CC DR PROSITE: PS00120; LIPASE_SER; 1.
 CC KM Hydrolyase; Lipid degradation; Signal; Calcium; 3D-structure.
 CC FT SIGNAL. 1 39
 CC FT CHAIN 40 358
 CC FT ACT_SITE 126 126 LIPASE.
 CC FT ACT_SITE 302 302 CHARGE RELAY SYSTEM.
 CC FT ACT_SITE 324 324 CHARGE RELAY SYSTEM.
 CC FT DISULFID 229 308
 CC FT MUTAGEN 54 54
 CC FT MUTAGEN 126 126 H->A: NO LOSS OF ACTIVITY.
 CC FT MUTAGEN 160 160 S->A: COMPLETE LOSS OF ACTIVITY.
 CC FT MUTAGEN 160 160 D->E: NO LOSS OF ACTIVITY.
 CC FT MUTAGEN 160 160 D->A: NO LOSS OF ACTIVITY.
 CC FT MUTAGEN 280 280 D->E: NO LOSS OF ACTIVITY.
 CC FT MUTAGEN 280 280 D->A: COMPLETE LOSS OF ACTIVITY.
 CC FT MUTAGEN 302 302 D->E: NO LOSS OF ACTIVITY.

FT MUTAGEN 302 302 D->A: 75% LOSS OF ACTIVITY.
 FT MUTAGEN 324 324 H->A: COMPLETE LOSS OF ACTIVITY.
 FT CONFLICT 40 40 A->W (IN REF. 2).
 SQ SEQUENCE 358 AA: 36928 MW: FEB75D/AZ22EC64B CRC64;
 Query Match 12.8%; Score 139.5; DB 1; Length 358;
 Best Local Similarity 29.6%; Pred. No. 0.00014;
 Matches 48; Conservative 26; Mismatches 59; Indels 29; Gaps 8;
 OY 1 MKVKRRIIALVILVSTSL-----FAMQPSAKAE-----HNPVNMHGIGASY 48
 Db 2 VRSMRSRVAAVAMALVAPLAGAGLTMAASPAADVATATRYPIVLVHGLGSTD- 60
 OY 49 NFA-----GIKSYLVSGWSRKGILVAND---FMDKTGTNNNGPYLSRFVOKVIDETG 98
 Db 61 KFAINVDMYWGIGDLSHSG---AKYVAVNLGSGFSDGPN-GRGELLAYVAVQVLAATG 116
 OY 99 AKKVDIVAHSMGAMTPYITKNDGKNKIEENVTLGANSST 140
 Db 117 ATKVNLIHSGGLTSRYVA--AVAPOLVASVTTIGTPHRGS 156
 RESULT 3
 LIP_BURCE STANDARD: PRT; 364 AA.
 ID LIP_BURCE
 AC P22088;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lipase precursor (EC 3.1.1.3) (Triacylglycerol lipase).
 GN LIP.
 OS Burkholderia cepacia (Pseudomonas cepacia).
 OC Bacteria: Proteobacteria; beta subdivision; Burkholderia group;
 OC Burkholderia.
 OX NCBI_TaxId=292;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 45-66.
 RX STRAIN=DSM 3959;
 RA MEDLINE=91100343; PubMed=1987151;
 RA Joergensen S., Skov K.W., Diderichsen B.;
 RA "Cloning, sequence, and expression of a lipase gene from Pseudomonas
 cepacia: lipase production in heterologous hosts requires two
 pseudomonas genes.";
 RT J. Bacteriol. 173:559-567(1991).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RX MEDLINE=97184684; PubMed=9032073;
 RA Kim K.K., Song H.K., Shin D.H., Hwang K.Y., Suh S.W.;
 RA "The crystal structure of a triacylglycerol lipase from Pseudomonas
 cepacia reveals a highly open conformation in the absence of a bound
 inhibitor.";
 RT Structure 5:173-185(1997).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=97184685; PubMed=9032074;
 RA Schrag J.D., Li Y., Cygler M., Lang D., Burgdorf T., Hecht H.-J.,
 RA Schmid R., Schomburg D., Rydel T.J., Oliver J.D., Strickland L.C.,
 RA Dunaway C.M., Larson S.B., Day J., McPherson A.O.;
 RA "The open conformation of a Pseudomonas lipase.";
 RT Structure 5:187-202(1997).
 RN [4]
 RP CATALYTIC ACTIVITY: triacylglycerol + H(2)O = diacylglycerol + a
 fatty acid anion.
 CC -1- COFACTOR: REQUIRES CALCIUM.
 CC -1- SIMILARITY: BELONGS TO THE AB HYDROLASE SUPERFAMILY. PSEUDOMONAS
 LIPASE FAMILY.
 CC -1- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
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 CC EMBL: M58494; AAA50466.1; -
 CC PIR: A39133; A39133.
 DR PDB: 1O1L; 15-MAR-97.
 DR PDB: 2LIP; 12-MAR-97.
 DR PDB: 3LIP; 16-JUN-97.
 DR InterPro: IPR000073; Abhydrolase.
 DR InterPro: IPR000734; Lipase.
 DR InterPro: IPR000379; Ser-estrs_site.
 DR Pfam: PF00561; abhydrolase_1.
 DR PROSITE: PS00120; LIPASE_SER; 1.
 KW Hydrolyase; Lipid degradation; Signal; Calcium; 3D-structure.
 FT CHAIN 1 44
 FT SIGNAL 1 44
 FT ACT_SITE 131 131
 FT ACT_SITE 286 286
 FT ACT_SITE 330 330
 SQ SEQUENCE 364 AA: 37494 MW: E9CD2DFB55658E9 CRC64;
 Query Match 11.5%; Score 125; DB 1; Length 364;
 Best Local Similarity 28.2%; Pred. No. 0.0024;
 Matches 40; Conservative 27; Mismatches 51; Indels 24; Gaps 8;
 OY 14 ILVLSVT--SLFAMQPSA-KAENHPVNMVHGIGASYNFAGIKSYLVSGM----- 62
 Db 29 VMTLATTHAMAMADPAAGAAATRYPIVLVHGLGSTD-KYAGVLEY-----WVGIGEDLD 82
 OY 63 -SGKGLVAND---FMDKTGTNNNGPYLSRFVOKVIDETGAKKVDIVAHSMGAMTPYIT 118
 Db 83 QNCATVYVAVNLGSGFSDGPN-GRGELLAYVAVQVLAATGATRVNLIHSGGLTSRYVA 141
 OY 119 KNDGKNKIEENVTLGANSST 140
 Db 142 --AVAPDLVASVTTIGTPHRGS 161
 RESULT 4
 LIP_VIBCH STANDARD: PRT; 312 AA.
 ID LIP_VIBCH
 AC P15493; O07349; Q9KRM7;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactonizing lipase precursor (EC 3.1.1.3) (Triacylglycerol lipase).
 GN LIPA OR HLVC OR VCA0221.
 OS Vibrrio cholerae.
 OC Bacteria: Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxId=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=El Tor O17 / Serotype O1;
 RX MEDLINE=90286918; PubMed=2162464;
 RA Alm R.A., Manning P.A.;
 RA "Characterization of the hlyB gene and its role in the production of
 the El Tor haemolysin of *Vibrio cholerae* O1.";
 RT Mol. Microbiol. 4:413-425(1990).
 RN [2]
 RP IDENTIFICATION AND REVISIONS.
 RC STRAIN=El Tor O17 / Serotype O1;
 RA Manning P.A.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=El Tor N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heideberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Uitterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;

RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae." ;
CC Nucleotide: 406:477-483(2000).
CC -1- FUNCTION: CATALYZES THE SYNTHESIS OF MACROCYCLIC LACTONES IN
CC ANHYDROUS ORGANIC SOLVENTS.
CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -1- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
CC -----
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CC -----
DR EMBL: Y00557; CAA68639.1; -
DR EMBL: AE004362; AAF96133.1; ALT_INIT.
DR PIR: S08007; S08007.
DR PIR: S15911; S15911.
DR HSSP: P22088; 3LIP.
DR TIGR: VCA0221; -
DR InterPro: IPR000073; Abhydrolase.
DR InterPro: IPR000734; Lipase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00561; abhydrolase; 1.
DR PROSITE: PS00120; LIPASE_SER; 1.
DR HydroLase: Lipid degradation; Signal; Complete proteome.
KW CHAIN 1 22
FT SIGNAL 1 22
FT CHAIN 23 312 LACTONIZING LIPASE.
FT ACT_SITE 110 110 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 238 238 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 278 278 CHARGE RELAY SYSTEM (BY SIMILARITY).
SQ SEQUENCE 312 AA; 32995 MW; 96AA000A07A568CD CRC64;

Query Match 11.4%; Score 124.5; DB 1; Length 312;
Best Local Similarity 26.9%; Pred. No. 0.0022;
Matches 43; Conservative 31; Mismatches 67; Indels 19; Gaps 8;

OY 7 RIILALVTLVLSV-----TSLFAMOPSARAKAEHNPNVWVG-----IGGASYNFGRS 55
DB 3 KIILIALSLFSSSIWATSAHALSQOQYQTRVIVLVHGLFGFDLAGMDY-FHGIPO 61
OY 56 YLVSGMSRGLVAVDEMDKTGTNNNGPVLSEFQVYLDGTAKKVDIVAHSMGANTP 115
DB 62 SLTRDGG--AQVYVAQV-SATNSSRERCEQLLAQVESLAVTGAKKVLIGHSHGCP-TI 116
OY 116 YIKNLGDKNKIENVVTLGGANR-STTSKALPGTDPNOKI 154
DB 117 RYVASV-RPDLVASVSTIGVHGSAVADLVGRVPSGSV 155

RESULT 5
LIP_PSES5 STANDARD; PRT; 364 AA.
ID LIP_PSES5
AC P25275;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE LIPase precursor (EC 3.1.1.3) (Triacylglycerol lipase).
GN LIP.
OS Pseudomonas sp. (strain KWI-56).
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=311;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 45-47.
RX MEDLINE=92118326; PubMed=1368739;
RA Iizumi T., Nakamura K., Shimada Y., Sugihara A., Tomimaga Y.,
RA Fukase T.;
RT "Cloning, nucleotide sequencing, and expression in Escherichia coli
RT of a lipase and its activator genes from Pseudomonas sp. KWI-56.";

RL Agric. Biol. Chem. 55:2349-2357(1991).
CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
CC fatty acid anion.
CC -1- SIMILARITY: BELONGS TO THE AB HYDROLASE SUPERFAMILY. PSEUDOMONAS
CC LIPASE FAMILY.
CC -1- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D10069; BAA00960.1; -
DR EMBL: S77842; AAC60400.1; -
DR PIR: J01227; J01227.
DR PIR: J01227; J01227.
DR HSSP: P22088; 3LIP.
DR InterPro: IPR000073; Abhydrolase.
DR InterPro: IPR000734; Lipase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00561; abhydrolase; 1.
DR PROSITE: PS00120; LIPASE_SER; 1.
DR HydroLase: Lipid degradation; Signal.
KW CHAIN 1 44
FT SIGNAL 1 44
FT CHAIN 45 364 LIPASE.
FT ACT_SITE 131 131 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 286 286 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 330 330 CHARGE RELAY SYSTEM (BY SIMILARITY).
SQ SEQUENCE 364 AA; 37511 MW; F346CB8B2E94E27D CRC64;

Query Match 11.2%; Score 122; DB 1; Length 364;
Best Local Similarity 25.3%; Pred. No. 0.0043;
Matches 42; Conservative 28; Mismatches 58; Indels 38; Gaps 8;

OY 4 VKRIIALVTLVLSV-----TSLFAMOPSARAKAEHNPNVWVGIGCA 46
DB 5 MRSRVAGAVACANSIAPFACTTAVMTLATVHAAMATAPADGYAATVTPITLVHGSLGT 64
OY 47 SYNFAGISYLVSGW-----SRGLIAYVD--FMDRTGTNNNGPVLSEFQVY 94
DB 65 D-KYAGVYEV-----WYIOEDLDQNGATVYVNLGSGQSDGDN-GEGBEDLLAVYKIVL 117
OY 95 DETGAKKVDIVAHSMGANTPYIKNLGDKNKIENVVTLGGANST 140
DB 118 AATGATKVNVLVHGSGGLTSRYVA--AAAPDLVASVTITGPHRGS 161

RESULT 6
ESL2_MYCPN STANDARD; PRT; 268 AA.
ID ESL2_MYCPN
AC P75311;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative esterase/lipase 2 (EC 3.1.1.3).
GN MPN473 OR MP368.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;
RX MEDLINE=97105885; PubMed=8948633;
RA Himmelreich R., Hilbert H., Plagens H., Plökl E., Lö B.-C.,
RA Herrmann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae." ;
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -1- SIMILARITY: BELONGS TO THE LIP3/BCHO FAMILY OF LIPASES/ESTERASES.
CC -----

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 CC or send an email to license@sib-sib.ch).

CC -----
 DR EMBL: AE000035; AAB96016.1; -
 DR InterPro: IPR000073; Abhydrolase.
 DR InterPro: IPR000379; Ser-ester- site.
 DR Pfam: PF00561; abhydrolase_1.
 DR Hypothetical protein; Hydrolase; Serine esterase; Complete proteome.
 FT ACT_SITE 28 28
 FT ACT_SITE 96 96 POTENTIAL.
 FT ACT_SITE 28 28 CHARGE RELAY SYSTEM (BY SIMILARITY).
 SQ SEQUENCE 268 AA: 30784 MW: 29D5F87E12090C9B CRC64;

Query Match 9.0%; Score 97.5; DB 1; Length 268;
 Best Local Similarity 32.7%; Pred. No. 0.34;
 Matches 32; Conservative 14; Mismatches 39; Indels 13; Gaps 6;

QY 21 SIFAMPSSKAHNPVWVHGGSGSYNFAIGKSYLVSGWRGKLVAVDFDKTGVY 80
 DB 11 SIFAFPHRK--RHN-FIFLHGSGSEYSSFKHFKLEKKRMS--FFAFNF-PGHGNNQ 63
 QY 81 NNGP---VLSRFVQKVL---ETGAKKVDIVAHSMGA 112
 DB 64 SNSVDLKKHYELVCDFTIOLKRLKKVVLVGHSMGA 101

RESULT 7
 LIP_STAEP STANDARD: PRT: 688 AA.
 ID LIP_STAEP
 AC 002510;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lipase precursor (EC 3.1.1.3) (Glycerol ester hydrolase).
 DE GENC.
 OS Staphylococcus epidermidis.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1282;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 303-315.
 RC STRAIN=9;
 RX MEDLINE=93171870; PubMed=8436947;
 RA Farrell A.M., Foster T.J., Holland K.T.;
 RT "Molecular analysis and expression of the lipase of Staphylococcus
 RT epidermidis";
 RL J. Gen. Microbiol. 139:267-277(1993).
 CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a
 CC fatty acid anion.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MISCELLANEOUS: THE EXPRESSION OF STAPHYLOCOCCUS LIPASE IS
 CC NEGATIVELY REGULATED BY BACTERIOPHAGE LYSOGENIZATION (LIPASE
 CC CONVERSION).
 CC -1- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
 CC -----
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CC -----
 DR EMBL: M95577; AAA19729.1; -
 DR PIR: A47705; A47705.
 DR InterPro: IPR000734; Lipase.
 DR InterPro: IPR000379; Ser-ester- site.
 DR TIGRfam: TIGR01168; YSIRK signal; 1.
 DR PROSITE: PS00120; LIPASE_SER; 1.
 KW Hydrolase; Lipid degradation; Zymogen; Signal.

FT SIGNAL 1 35 POTENTIAL.
 FT PROPEP 36 302 REMOVED IN THE MATURE FORM.
 FT CHAIN 303 688 LIPASE.
 FT ACT_SITE 418 418 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 648 648 CHARGE RELAY SYSTEM (BY SIMILARITY).
 SQ SEQUENCE 688 AA: 77198 MW: 70A92EF25834B9E31 CRC64;

Query Match 8.6%; Score 94; DB 1; Length 688;
 Best Local Similarity 19.7%; Pred. No. 2.1;
 Matches 46; Conservative 36; Mismatches 61; Indels 90; Gaps 11;

QY 28 SAKAAEH---NPVWVHGGSGSYNFAIGKSYLVSGWRGKLVAVDFDKTGVY 71
 DB 301 SAKQKQYKNNPDPIIVHGFNGFTD---INPSVLTHTYWGDKNNINQDLEENGEAYEAS 357
 QY 72 FMDKTGTNNNGVYLSRFVQKVLDEFGA-----KKVDIYA 106
 DB 358 I-SAFGSNDRAVELYYIKGRVYGAHAHAARYGKTYGVYKDMKPKQKTHLVG 416
 QY 107 HSMGKAN-----TPYITKNDGG--NKIENVYTLGAMR 138
 DB 417 HSMGGTTIOLEHLRHGNPEVEYKQNGEISPL-----QGCHDMVTSITTLGTPIN 472
 QY 139 STTSKALPCTDPNOKITLYTSYSSADMIYNNYLSKLDGAKNAOI-HGVCHIGL 190
 DB 473 GTHASDLTG---NEAIVROLAYD-----VGKMYGNKDSRVDEGLHWMGL 513

RESULT 8
 ACOC_ALCEU STANDARD: PRT: 373 AA.
 ID ACOC_ALCEU
 AC P27747;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Dihydrolipoamide acetyltransferase component of acetoacetyl
 DE system (EC 2.3.1.12) (Acetoacetyl dehydrogenase E2 component)
 DE (Fast-migrating protein) (FMP).
 DE ACOC.
 OS Alcaligenes eutrophus (Ralstonia eutropha).
 OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
 OC Ralstonia.
 OX NCBI_TaxID=510;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-27.
 RC STRAIN=H16 / DSM 428 / ATCC 17699;
 RX MEDLINE=91286190; PubMed=2061286;
 RA Priefer H., Hein S., Kruenger N., Zeh K., Schmidt B., Steinbuechel A.;
 RT "Identification and molecular characterization of the Alcaligenes
 RT eutrophus H16 acetoacetyl genes involved in acetoacetyl catabolism";
 RL J. Bacteriol. 173:4056-4071(1991).
 CC -1- FUNCTION: DIHYDROLIPOAMIDE ACETYLTRANSFERASE INVOLVED IN
 CC ACETOIN CATABOLISM.
 CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide = CoA + S-
 CC acetylhydrolipoamide.
 CC -1- COFACTOR: THE E2 COMPONENT CONTAINS ONE COVALENTLY-BOUND LIPOYL
 CC COFACTOR (PROBABLE).
 CC -1- PATHWAY: Acetoacetyl catabolism.
 CC -1- INDUCTION: BY GROWTH ON ACETOIN.
 CC -1- SIMILARITY: CONTAINS 1 LIPOYL-BINDING DOMAIN.
 CC -----
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CC -----
 DR EMBL: M60600; AAA21950.1; -
 DR PIR: DA2462; DA2462.
 DR HSP: P20706; 1GHR.
 DR InterPro: IPR003089; AB_hydrolase.

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DR InterPro: IPR000073; Abhydrolase.
DR InterPro: IPR000089; Biotin_lipoyl.
DR InterPro: IPR003016; Lipoyl.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00364; biotin_lipoyl.1.
DR Pfam: PF00561; abhydrolase.1.
DR PRINTS: PR00111; ABHYDROLASE.
DR PROSITE: PS00189; Lipoyl.1.
DR Transferase; Acyltransferase; Lipoyl.
FT BINDING 49 49 0
FT INT_MET 0
SQ SEQUENCE 373 AA; 38904 MM; 905CELF83E94892F CRC64;

Query Match 8.1%; Score 88.5; DB 1; Length 373;
Best Local Similarity 20.7%; Pred. No. 2.9;
Matches 40; Conservative 36; Mismatches 76; Indels 41; Gaps 8;

OY 37 VMMVHGIGGASVY-----FAGIKSYLVSGMSNGKLYAVDFMDKNTNNNGPV 85
DB 137 VLEHFGEGDLDNMLFNLDPADATVVALDLPGHGSSPRL-----AGTTLAQ--- 185
OY 86 LSREYQKVLDETGAKKVDIVAHSMGCAATPYIKMLDGNKLENY-----VTLGANRST 140
DB 186 MAGFARFARMEDEGIEAAHVGHSGMGVAAQLA--VDAPORLSVALVSPVGFDAVNSG 243
OY 141 TSKALPGDPPNOKT--LYTSIYSSADMVVMNYLSKLDGAKNAQHGVGHIGLLMSQVNS 198
DB 244 YTEGFVSAQSRRLEKPVVELLFADAGLVSRMLDDL--LRYKRLDGV-----TEALT 293
OY 199 LIKEGLNGGGONT 211
DB 294 ALGGGLPFGGGRS 306

RESULT 9
LIP_PSEAE
ID LIP_PSEAE STANDARD; PRT; 311 AA.
AC P36876;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lactonizing lipase precursor (EC 3.1.1.3) (Triacylglycerol lipase).
GN LIP OR LIPA OR PA2862.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
CC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAOI;
RX MEDLINE=92381478; PubMed=1512563;
RA Wohlfarth S., Hoesch C., Strunk C., Winkler U.K.;
RT "Molecular genetics of the extracellular lipase of Pseudomonas aeruginosa PAOI."
RL J. Gen. Microbiol. 138:1325-1335(1992).
RN [2]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC STRAIN=TE3285;
RX MEDLINE=92337414; PubMed=1632642;
RA Chihara-Sioml M., Yoshikawa K., Oshima-Hirayama N., Yamamoto K.,
RA Sogabe Y., Nakatani T., Nishiooka T., Oda J.;
RT "Purification, molecular cloning, and expression of lipase from Pseudomonas aeruginosa."
RL Arch. Biochem. Biophys. 296:505-513(1992).
RN [3]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 27-57.
RC STRAIN=PAOIR;
RX MEDLINE=92247813; PubMed=1576157;
RA Jaeger K.E., Adrian F.-J., Meyer H.E., Hancock R.E.W., Winkler U.K.;
RT "Extracellular lipase from Pseudomonas aeruginosa is an amphiphilic protein."
RL Biochim. Biophys. Acta 1120:315-321(1992).
RN [4]

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RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAOI;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brickman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Laidig R.M.,
RA Smilt L.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an opportunistic pathogen."
RL Nature 406:959-964(2000).
RN [5]
RP SEQUENCE OF 28-39.
RC STRAIN=EF2;
RX MEDLINE=92085040; PubMed=1748875;
RA Gilbert E.J., Cornish A., Jones C.W.;
RT "Purification and properties of extracellular lipase from Pseudomonas aeruginosa EF2."
RL J. Gen. Microbiol. 137:2223-2229(1991).
CC -1- FUNCTION: CATALYZES THE SYNTHESIS OF MACROCYCLIC LACTONES IN ANHYDROUS ORGANIC SOLVENTS.
CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O -> diacylglycerol + a fatty acid anion.
CC -1- SUBCELLULAR LOCATION: DURING EARLY STATIONARY GROWTH PHASE ABOUT 10% OF THE ENZYME MOLECULES REMAIN CELL-BOUND WHILE ABOUT 90% ARE RELEASED INTO THE GROWTH MEDIUM.
CC -1- MISCELLANEOUS: LIPASE OF STRAIN EF2 EXHIBITS SOME ESTERASE ACTIVITY, AND SHOWS A MARKED SPECIFICITY OR THE 1,3-OLEYL RESIDUES OF TRIOLEIN.
CC -1- SIMILARITY: BELONGS TO THE AB HYDROLASE SUPERFAMILY. PSEUDOMONAS LIPASE FAMILY.
CC
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CC
DR EMBL: X63390; CAA44997.1; -
DR EMBL: AB008452; BAA23128.1; -
DR EMBL: AX000441; CAB77076.1; -
DR EMBL: AE004712; AAG06250.1; -
DR PIR: S25768; S25768.
DR PIR: S24160; S24160.
DR HSSP: P22088; 3ILP.
DR InterPro: IPR000073; Lipase.
DR InterPro: IPR000734; Abhydrolase.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF00561; abhydrolase.1.
DR PROSITE: PS00120; LIPASE_SER; 1.
KW Hydrolase; Lipid degradation; Signal; Complete proteome.
FT SIGNAL 1 26
FT CHAIN 27 311
FT ACT_SITE 108 108
FT ACT_SITE 235 235
FT ACT_SITE 277 277
FT VARIANT 33 33 K -> Q (IN STRAIN EF2).
FT VARIANT 156 156 V -> I (IN STRAIN TE3285).
FT VARIANT 202 202 Q -> H (IN STRAIN TE3285).
FT VARIANT 204 204 I -> V (IN STRAIN TE3285).
SQ SEQUENCE 311 AA; 32723 MM; 7DB1ADF27BDE5619 CRC64;

Query Match 8.1%; Score 88; DB 1; Length 311;
Best Local Similarity 28.8%; Pred. No. 2.6;
Matches 32; Conservative 19; Mismatches 46; Indels 14; Gaps 5;

OY 15 LVLSVTSIFA--MPSAKAAEHNPVWVHG-----IGCASYNFAGIKSYLVSGMSRG 65
DB 11 LAIGLASIAASPLIDASITYTQTKYPIVLAHGMGLGDNILGVDMF--GIPSLARRDG---A 66

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OY 66 KLYAVDFMDKTGTNNNGPVLRSFVOKVDETGAKKVDIVAHSMGSGANTPY 116
 DB 67 QYVYVEV-SQLDTSEYRGEGQLLOQVEIYALSGQPKVNLIGHSHGPTIRY 116

RESULT 10
 LIP_PSESP STANDARD: PRT: 311 AA.
 AC P26677:
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lactonizing lipase precursor (EC 3.1.1.3) (Triacylglycerol lipase).
 GN LIP.
 OS Pseudomonas sp. (strain 109).
 OC Bacteria; Proteobacteria.
 OX NCBI_TaxID=306;
 RN (1)
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-45.
 RX MEDLINE=92011544; PubMed=1917947;
 RA Ihara F., Kageyama Y., Hirata M., Nihira T., Yamada Y.;
 RT "Purification, characterization, and molecular cloning of lactonizing lipase from Pseudomonas species";
 RL J. Biol. Chem. 266:18135-18140(1991).
 CC -1- FUNCTION: CATALYZES THE SYNTHESIS OF MACROCYCLIC LACTONES IN ANHYDROUS ORGANIC SOLVENTS.
 CC -1- CATALYTIC ACTIVITY: Triacylglycerol + H(2)O = diacylglycerol + a fatty acid anion.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE AB HYDROLASE SUPERFAMILY. PSEUDOMONAS LIPASE FAMILY.
 CC -1- SIMILARITY: BELONGS TO THE ABHYDROLASE SUPERFAMILY. LIPASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: D10166; BAA01035.1; -
 DR PIR: A40943; A40943.
 DR HSSP: P22088; 3LIP.
 DR InterPro: IPR000073; Abhydrolase.
 DR InterPro: IPR000734; Lipase.
 DR InterPro: IPR000379; Ser_estr_ site.
 DR Pfam: PF00561; abhydrolase_1.
 DR ProSITE: PS00120; LIPASE_SER; 1.
 DR KEGG: Hydrolase; Lipid degradation; Signal.
 FT SIGNAL 1 26
 FT CHAIN 27 311 LACTONIZING LIPASE.
 FT ACT_SITE 108 108 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 235 235 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 277 277 CHARGE RELAY SYSTEM (BY SIMILARITY).
 SQ SEQUENCE 311 AA: 32737 MW; 27AC2F3DB334D1 CRC64;

Query Match 8.1%; Score 88; DB 1; Length 311;
 Best Local Similarity 28.8%; Pred. No. 2.6;
 Matches 32; Conservative 19; Mismatches 46; Indels 14; Gaps 5;

OY 15 LVLSVTSLEFA--MPSAKAEHNPVVMVHG-----IGASYNFAGIKSYLVSGMSG 65
 DB 11 LAIGLASLASPLQIAGSTYTGKRYPIVLAHGMFGFNDILGVDYWF-GISALRRDQ---A 66
 OY 66 KLYAVDFMDKTGTNNNGPVLRSFVOKVDETGAKKVDIVAHSMGSGANTPY 116
 DB 67 QYVYVEV-SQLDTSEYRGEGQLLOQVEIYALSGQPKVNLIGHSHGPTIRY 116

RESULT 11
 YEGM_ECOLI STANDARD: PRT: 415 AA.
 ID YEGM_ECOLI

AC P76397;
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein yegm precursor.
 GN YEGM OR B2074.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12";
 RL Science 277:1453-1474(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97251358; PubMed=9097040;
 RA Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Maki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y., Sivasubram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horuchi T.;
 RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map";
 RL DNA Res. 3:379-392(1996).
 CC -1- SIMILARITY: BELONGS TO THE ACRA/ACRE FAMILY.
 CC -----
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 CC -----
 DR EMBL: AE000297; AAC75135.1; ALT_INIT.
 DR EMBL: D90845; BAA15928.1; ALT_INIT.
 DR EcoGene: EG14056; yegm.
 DR InterPro: IPR002215; H1YD.
 DR Pfam: PF00529; H1YD; 1.
 KW Hypothetical protein; Complete proteome.
 FT SIGNAL 1 21
 FT CHAIN 22 415 HYPOTHETICAL PROTEIN YEGM.
 FT SIGNAL 22 415
 SQ SEQUENCE 415 AA: 44464 MW; 26240DBEDDEIA5F CRC64;

Query Match 8.0%; Score 87.5; DB 1; Length 415;
 Best Local Similarity 25.4%; Pred. No. 4;
 Matches 36; Conservative 22; Mismatches 61; Indels 23; Gaps 5;

OY 58 VSGGWSRGKLVAVDFMDKTGT--NINNGPVLRSFVOKVLD-ETGAKKVDIVAHSMGSGANTP 115
 DB 248 VVOAQKAGRPPLVEADWDRTNSKKLSGTLSS--LDNQIDATGTGTVKARFNNQDDALFP 305
 OY 116 YVYKN-----LDGKNLEVVNTTGGANRSTSKALGTPNOKILYT 157
 DB 306 NOEVNARMVLVDTEQNAVITPTALQNGNGCHRYVWYVNLSENKYSKHLVYTGIDQSDQKVVIR 365
 OY 158 STYSSADMTVMYVLSKL-DGAK 178
 DB 366 AGISAGDRAVVTGIDRLTEGAK 387

RESULT 12
 Y045_MYCPN STANDARD: PRT: 485 AA.
 ID Y045_MYCPN

AC P75056;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical Lipoprotein MG045 homolog precursor (D09_orf485).
 GN MNR058 OR MP096.
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 NCBI_TaxID=2104;
 RX MEDLINE=97105885; PubMed=8948633;
 RA Himmelfeich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 pneumoniae.";
 RT Nucleic Acids Res. 24:4420-4449(1996).
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
 (Potential).
 CC -----
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 CC -----
 DR EMBL; AE000011; AAB95744.1;
 DR InterPro: IPR000044; LipProtL_MG045.
 DR Pfam: PF02030; Lipoprotein_8; 1.
 DR PRINTS; PR00905; MYC045.
 DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
 KW Hypothetical protein; Lipoprotein; Membrane; Signal;
 KM Complete proteome.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 485 HYPOTHETICAL LIPOPROTEIN MG045 HOMOLOG.
 FT LIPID 23 23 N-ACYL DIGLYCERIDE (POTENTIAL).
 SQ SEQUENCE 485 AA; 55019 MW; 1AD4E0AB211B64F8 CRC64;
 Query Match 8.0%; Score 87.5; DB 1; Length 485;
 Best Local Similarity 20.9%; Pred. No. 4.9;
 Matches 53; Conservative 34; Mismatches 100; Indels 67; Gaps 9;
 QY 2 KFYRRITATVITVSVTSIFAMOPSAKAAEHNVVWVHGIGASVNFACIKSYLSOG 61
 DB 27 QFVANESESYSPLLERAE--AKQPMFTLYPTNEKLIINGFANNVTYVAASVASEL 84
 QY 62 WSRGKIVAVDW---DKGTNNNGPVLSRFQKVLDEFGAKKVDVAHSMGANTPY 116
 DB 85 QQQGHLLPID-WAKFNLLKKTGNSQATONKEDK--ELFTKEIGDISGLLWGVY 140
 QY 117 YIKNI---DGNKILNVVTLGANSRSTSKALPTDPNOKILYTSIVSSAMIVNYLSK 173
 DB 141 FLQDLVEVYRGEKIOE-----LEGQDVWSTIIKAIVHKRPNRNLAL 185
 QY 174 LDGAK-----NAQIHG-----GHG-----LLMSQ 195
 DB 186 IDDRRTIFSLANVHHEKNTTVVNPSTGLNFGVYESFANGLKRDNLNTLFVNSD 245
 QY 196 VNSLIKEGLNGGQ 209
 DB 246 SNIITNELANGRRQ 259
 RESULT 13
 ID BNIL YEAST STANDARD; PRT; 1953 AA.
 AC P41832;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE BNIL protein (Synthetic lethal 39).
 GN BNIL OR SHE5 OR YNL271C OR N0646.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fares H.F., Pringle J.R.;
 RT "Synthetic lethals of CDC12.";
 RL Submitted (XXX-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1-1553 FROM N.A.
 RC STRAIN=5288C / FY1679;
 RX Sen-Gupta M., Lyck R., Fleig U., Niedenthal R.K., Hegemann J.H.;
 RT "The sequence of a 24,152 bp segment from the left arm of chromosome
 RT XIV from Saccharomyces cerevisiae between the BNIL and the POL2
 RT genes.";
 RL Yeast 12:505-514(1996).
 RL [3]
 RP SEQUENCE OF 988-1953 FROM N.A.
 RA Messenguy F., Dubois E., Vierendeels F., Scherens B., Pierard A.,
 RA Glandsdorf N.;
 RN Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP FUNCTION.
 RX MEDLINE=99187130; PubMed=10085293;
 RA Lee L., Klee S.R., Evangelista M., Boone C., Pellman D.;
 RT "Control of mitotic spindle position by the Saccharomyces cerevisiae
 RT formin Bnlp.";
 RL J. Cell Biol. 144:947-961(1999).
 CC -1- FUNCTION: MAY ORGANIZE MICROTUBULES BY MEDIATING SPINDLE
 CC POSITIONING AND MOVEMENT IN THE BUDDING PROCESS. POTENTIAL TARGET
 CC OF THE RHO FAMILY MEMBERS.
 CC -1- SUBUNIT: INTERACTS WITH PROFILIN AT THE FHL DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 GTPASE-BINDING DOMAIN (GBD).
 CC -1- SIMILARITY: CONTAINS 1 FORMIN HOMOLOG 1 (FHL) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 FORMIN HOMOLOG 2 (FH2) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 FORMIN HOMOLOG 3 (FH3) DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 DRF AUTOREGULATORY DOMAIN (DAD).
 CC -1- SIMILARITY: BELONGS TO THE FORMIN HOMOLOG FAMILY. BNIL
 CC SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; L31766; AAA34455.1;
 DR EMBL; 271546; CA96178.1;
 DR EMBL; 271547; CA96179.1;
 DR EMBL; X92494; CA63225.1;
 DR SGD; S0005215; BNIL.
 DR InterPro: IPR003104; FH2.
 DR Pfam; PF02181; FH2; 1.
 DR SMART; SM00498; FH2; 1.
 KW Colled coil.
 FT DOMAIN 123 504 GBD.
 FT DOMAIN 356 723 FH3.
 FT DOMAIN 712 807 COILED COIL (POTENTIAL).
 FT DOMAIN 864 894 COILED COIL (POTENTIAL).
 FT DOMAIN 928 981 COILED COIL (POTENTIAL).
 FT DOMAIN 1053 1337 FHL (PRO-RICH).
 FT DOMAIN 1348 1824 FH2.
 FT DOMAIN 1732 1811 COILED COIL (POTENTIAL).
 FT DOMAIN 1799 1813 DAD.
 FT DOMAIN 64 67 POLY-SER.
 FT DOMAIN 1053 1057 POLY-SER.
 FT DOMAIN 1239 1250 POLY-PRO.

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OM protein - protein search, using sw model

Run on: May 9, 2003, 16:18:56 ; Search time 31 Seconds
(without alignments)
1409.096 Million cell updates/sec

Title: US-09-905-666A-55
Perfect score: 1088
Sequence: 1 MKFVRRRIALVTILVSVT.....NSQVNSLIKEGLINGSGONTN 212

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_21: *
1: sp-archaea: *
2: sp-bacteria: *
3: sp-fungi: *
4: sp-human: *
5: sp-invertebrate: *
6: sp-mammal: *
7: sp-mhc: *
8: sp-organelle: *
9: sp-phage: *
10: sp-plant: *
11: sp-rodent: *
12: sp-virus: *
13: sp-vertebrate: *
14: sp-unclassified: *
15: sp-virus: *
16: sp_bacteriap: *
17: sp-archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	771.5	70.9	215	2 Q8VU78	Q8VU78 bacillus sp
2	751	69.0	181	2 Q9K5F4	Q9K5F4 bacillus li
3	731.5	67.2	210	16 P94444	P94444 bacillus sp
4	719.5	66.1	210	2 Q8RJP5	Q8RJP5 bacillus me
5	208	19.1	237	16 Q9RSP6	Q9RSP6 delinococcus
6	181.5	16.7	331	16 Q9KY65	Q9KY65 streptomyces
7	178	16.4	290	16 Q9S295	Q9S295 streptomyces
8	173.5	15.9	403	16 Q8RC83	Q8RC83 thermococcus
9	160.5	14.8	339	2 Q59644	Q59644 propionibac
10	153.5	14.1	202	16 P73372	P73372 synchocyst
11	152	14.0	275	2 Q33969	Q33969 streptomyces
12	149	13.7	286	5 Q9NAK4	Q9NAK4 caenorhabdi
13	148	13.6	291	14 Q91UY0	Q91UY0 uncultured
14	145.5	13.4	289	16 Q9K3H5	Q9K3H5 streptomyces
15	145	13.3	211	16 Q8YX63	Q8YX63 anabaena sp
16	142.5	13.1	344	5 Q23548	Q23548 caenorhabdi

17	139.5	12.8	300	5 Q19310	Q19310 caenorhabdi
18	137.5	12.6	371	5 Q22420	Q22420 caenorhabdi
19	131.5	12.1	474	17 Q28511	Q28511 archaeoglob
20	131	12.0	292	5 Q76556	Q76556 caenorhabdi
21	130	11.9	479	16 Q97K91	Q97K91 clostridium
22	129	11.9	300	16 Q92D71	Q92D71 listeria in
23	128.5	11.8	360	2 Q68551	Q68551 pseudomonas
24	125.5	11.5	171	2 Q56594	Q56594 vibrio chol
25	125.5	11.5	339	16 Q8XXN1	Q8XXN1 ralstonia s
26	123.5	11.4	329	5 Q22060	Q22060 caenorhabdi
27	121	11.1	323	2 Q43962	Q43962 acinetobact
28	121	11.1	333	5 Q20437	Q20437 caenorhabdi
29	120.5	11.1	290	2 Q52614	Q52614 proteus vul
30	119	10.9	340	5 Q16380	Q16380 caenorhabdi
31	116	10.7	309	2 P72172	P72172 pseudomonas
32	115.5	10.6	395	10 Q9AY57	Q9AY57 oryza sativ
33	115.5	10.6	335	5 Q17622	Q17622 caenorhabdi
34	115	10.6	309	16 Q9HU27	Q9HU27 pseudomonas
35	112.5	10.3	212	10 Q9AUS1	Q9AUS1 oryza sativ
36	111	10.2	488	16 Q922Y5	Q922Y5 rhizobium m
37	109	10.0	281	5 Q19462	Q19462 caenorhabdi
38	108	9.9	380	2 Q93909	Q93909 pseudomonas
39	107	9.8	277	5 Q17376	Q17376 pseudomonas
40	106	9.7	497	16 Q9KBN0	Q9KBN0 bacillus ha
41	104.5	9.6	299	16 Q8Y8F4	Q8Y8F4 listeria mo
42	104	9.6	414	16 Q8R7S7	Q8R7S7 thermococcus
43	103.5	9.5	237	5 Q9NAK1	Q9NAK1 caenorhabdi
44	102	9.4	207	2 Q9EVC9	Q9EVC9 chloroflexu
45	102	9.4	237	2 Q9EVC8	Q9EVC8 chloroflexu

ALIGNMENTS

RESULT 1

Q8VU78 PRELIMINARY: PRT; 215 AA.
AC Q8VU78;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Lipase.
OS Bacillus sp. B26.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI:TaxID=117494;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B26;
RA Kim M.H., Kim H.K., Oh T.K., Lee J.K.;
RT "Cloning and sequencing of a lipase gene from Bacillus sp. B26";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF232707; AAL36938.1; -
DR InterPro: IPR002918; Lipase_2.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF01674; Lipase_2; 1.
SQ SEQUENCE 215 AA; 22959 MW; 460397D7026A789B CRC64;

Query Match	Score	771.5; DB 2;	Length	215;
Best Local Similarity	70.7%;	Pred. No. 4.6e-53;		
Matches 152; Conservative 26; Mismatches 34; Indels 3; Gaps 2;				
QY 1 MKFV--KRRIALVTILVSVTSLFMP--SAKAAEHNPVYVHGAGSYNFAKISYL 57	11	11	11	11
Db 1 MKFVRRRIALVTILVSVTSLFMP--SAKAAEHNPVYVHGAGSYNFAKISYL 60	11	11	11	11
QY 58 VSGWGRGLYAVDFWDTGTNTNNGPVLRFVQKVLDETGAARVDIVAHSMGANTPY 117	11	11	11	11
Db 61 VSGWGRGLYAVDFWDTGTNTNNGPVLRFVQKVLDETGAARVDIVAHSMGANTPY 120	11	11	11	11
QY 118 IKMLDGNKTIENVVTLGGANRSTSKALRPTDQNKILITISYSSADMIYANLKLDDA 177	11	11	11	11
Db 121 IKMLDGNKTIENVVTLGGANRSTSKALRPTDQNKILITISYSSADMIYANLKLDDA 180	11	11	11	11


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Db      60  WGSNKLKLYAIDFYDKTGNNLNNGPQLASYDRLKFTGAKKVDIVAHSMGANTLYIKTL 119
Oy      122 DCGNKTIENVVTLGGANKRSTTSKALPCTDPNOKILYTSISSADMIYMYNLSKIDGAKNAQ 181
Db      120 GCGNKIQNVVTLGGANGLVSTALPCTDPNOKILYTSISLNDQIYINLSRLOGARNTQ 179
Oy      182 IHGVGHIGLMSQVNSLIKEGNGGONTN 212
Db      180 LYGIGHIGLMSQVNGYIKKGLNGGLMTN 210

RESULT 4
O9RJP5  PRELIMINARY; PRT; 210 AA.
ID      O9RJP5
AC      O9RJP5;
DT      01-JUN-2002 (TREMBlrel. 21, Created)
DT      01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE      01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE      Extracellular esterase precursor (EC 3.1.1.1).
GN      LIPA.
OS      Bacillus megaterium.
OC      Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC      Bacillaceae; Bacillus.
OX      NCBI_TaxID=1404;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=ATCC9885;
RA      Ruiz C., Pastor J., Diaz P.;
RT      "Identification and Cloning of Bacillus megaterium and Bacillus sp.
RT      BP-6 esterases. Comparison with Bacillus subtilis and Bacillus pumilus
RT      lipases."
RL      Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
DR      EMBL: AJ430831; CAD23620.1;
KM      Signal; Hydrolase.
FT      SIGNAL 1 28
FT      CHAIN 1 210
FT      SEQUENCE 210 AA; 22411 MW; 9408898826918 CRC64;
SO      POTENTIAL.
        EXTRACELLULAR ESTERASE.
        BEST LOCAL SIMILARITY 67.3%; PRED. NO. 5.5e-49;
        MATCHES 142; CONSERVATIVE 24; MISMATCHES 42; INDELS 3; GAPS 2;

Query Match 66.1%; Score 719.5; DB 2; Length 210;
Best Local Similarity 67.3%; Pred. No. 5.5e-49;
Matches 142; Conservative 24; Mismatches 42; Indels 3; Gaps 2;

Oy      4  VKRRIATVTLVSLVSLEFAMQPSAKAE--HNPVVMVHGIGGASYNFAGIKSYLVSOQ 61
Db      1  MKKVLMAFIICLSL-ILSYLAAPPAGKAKESVHNPPVVLVHGIGGASYNFPAIKNYLISOG 59
Oy      62  WSRGKIYAVDFDKTGTNNNGPVLRSFYQKYLDETGAKKVDIVAHSMGANTPYIKML 121
Db      60  WGSNKLKLYAIDFYDKTGNNLNNGPQLASYDRLKFTGAKKVDIVAHSMGANTLYIKTL 119
Oy      122 DCGNKTIENVVTLGGANKRSTTSKALPCTDPNOKILYTSISSADMIYMYNLSKIDGAKNAQ 181
Db      120 GCGNKIQNVVTLGGANGLVSTALPCTDPNOKILYTSISLNDQIYINLSRLOGARNTQ 179
Oy      182 IHGVGHIGLMSQVNSLIKEGNGGONTN 212
Db      180 LYGIGHIGLMSQVNGYIKKGLNGGLMTN 210

RESULT 5
O9RSP6  PRELIMINARY; PRT; 237 AA.
ID      O9RSP6
AC      O9RSP6;
DT      01-MAY-2000 (TREMBlrel. 13, Created)
DT      01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT      01-MAY-2000 (TREMBlrel. 20, Last annotation update)
DE      Lipase, putative.
GN      DR2078.
OS      Deinococcus radiodurans.
OC      Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
OC      Deinococcaceae; Deinococcus.
OX      NCBI_TaxID=1259;

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RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=R1;
RX      MEDLINE=20036896; PubMed=10567266;
RA      White O., Eissen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA      Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA      Moffat K.S., Qin H., Jiang L., Pamphile M., Crosby M., Shen M.,
RA      Vamathevan J.J., Lam P., McDonald L., Uitterback T., Zalewski C.,
RA      Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA      Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA      Fraser C.M.;
RT      "Genome sequence of the radioresistant bacterium Deinococcus
RT      radiodurans R1."
RL      Science 286:1571-1577(1999).
DR      EMBL: AE002044; AAF11628.1;
DR      TIGR: DR2078;
DR      InterPro: IPR002918; Lipase-2.
DR      InterPro: IPR000379; Ser_estrs_site.
DR      Pfam: PF01674; Lipase_2; 1.
KW      Complete proteome.
SO      SEQUENCE 237 AA; 25308 MW; 1C2BF99210B8AF2E CRC64;

Query Match 19.1%; Score 208; DB 16; Length 237;
Best Local Similarity 26.6%; Pred. No. 1.1e-08;
Matches 61; Conservative 47; Mismatches 93; Indels 28; Gaps 6;

Oy      1  MKPKRRIATVTLVSLVSLEFAMQPSAKAE-----HNPVVMVHGIGGASYNFAGIK 54
Db      6  LAFSKRFVLLPISALLACCGTITQAPSELDAQALAAPRHVPLFVHGFGNSDGSITWSPMM 65
Oy      55  SYLVSGWSRGKLYAVDFDKTGTNNNGPVLRSFYQKYLDETGAKKVDIVAHSMGANT 114
Db      66  NRRKQGWTDQALFMSY-DSEFSNAVPTADLRQKDALTAQGAQVQIVSHMSKALSS 124
Oy      115  PYIKNLDCGKTIENVVTLGGANR-----STTS-----KAL-PCTDPNOKI 154
Db      125  RYLLKMLGGTAKDAVWSLGGPNHGTDFALCASCIEBMROGSSPFIKALNSGDETPGAV 184
Oy      155  LYSIYSSADMIY-MNYLSKIDGAKNAQIHGVGHIGLMSQVNSLIKE 202
Db      185  RYATWMSPCDAVINPNSVPLSGATNTKTSCLTHSSLYGDATVYTYOVRD 233

RESULT 6
O9KY65  PRELIMINARY; PRT; 331 AA.
ID      O9KY65
AC      O9KY65;
DT      01-OCT-2000 (TREMBlrel. 15, Created)
DT      01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT      01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE      Putative secreted lipase.
GN      SC04799 OR SC063A.10C.
OS      Streptomyces coelicolor.
OC      Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC      Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomycetes.
OX      NCBI_TaxID=1902;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=A3(2);
RA      Brown S.P., Harris D.;
RL      Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=A3(2);
RA      Cerdano A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL      Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=A3(2);
RX      MEDLINE=97000351; PubMed=8643436;
RA      Redenbach M., Kieser H.M., Denapalte D., Eichner A., Cullum J.,
RA      Kinsahl H., Hopwood D.A.;
RT      "A set of ordered cosmids and a detailed genetic and physical map for

```

RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RT Mol. Microbiol. 21:77-96(1996).
RL [4]
RN
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdano-Parraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
Rabinowitsch E., Rajandream M.A., Rutherford K., Ruter S.,
Saunders K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,
Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL: AL356832; CAB92662.1; -
DR InterPro: IPR000734; Lipase.
DR InterPro: IPR000379; Ser_estrs_site.
DR PROSITE: PS00120; LIPASE_SER; 1.
SO SEQUENCE 331 AA; 35137 MW; 3E0E77A68747211 CRC64;

Query Match 16.78; Score 181.5; DB 16; Length 331;
Best Local Similarity 25.68; Pred. No. 2.1e-06;
Matches 54; Conservative 42; Mismatches 86; Indels 29; Gaps 6;

OY 27 PSAAAEHNPVVMVHGIGAGSYNFAIGKSYLVSGMSRGKLYAVDFMKTGTNNNGPVL 86
DB 106 PRPARAPRPVVLHGFIDNRSVFLRLSLAONG-RHAIESLVNSPLCTCIRTAELL 163
OY 87 SRFOVKVLEDFGAKKVDIVAHSMGANTPPYIKNDGKNKIENVVTLGANSRTSKAL- 145
DB 164 GRHIEICERGSEKRVGVHGLIARYVYORLGGDLRYFTLVLTGTPTGTGVVPLA 223
OY 146 -----GFT-----DPNQKILYTSVSSADMIYNNYLSK--LD-----GAKNA 180
DB -224 NAHPIVRQMRPESAVIEELTPRAPCCRTFRVSEFMSDLDR-VMDPLETACLDHPLDSOVN 282
OY 181 QIHGVGHIGLIMNSQVNSLIRKELNGGGGONT 211
DB 283 RVSGIGHLALPVHAPVATGIRQALDTAPPET 313

RESULT 7
O9S295 PRELIMINARY; PRT; 290 AA.
ID O9S295;
AC O9S295;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Putative secreted lipase.
GN SC01735 OR SC11.24C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Saunders D., Harris D.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapante D., Eichner A., Cullum J.,
Kinasht H., Hopwood D.A.;

RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RT Mol. Microbiol. 21:77-96(1996).
RL [4]
RN
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdano-Parraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
Rabinowitsch E., Rajandream M.A., Rutherford K., Ruter S.,
Saunders K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,
Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL: AL096849; CAB50950.1; -
DR HSSP; Q05489; 17AH.
DR InterPro: IPR002918; Lipase_2.
DR InterPro: IPR000379; Ser_estrs_site.
DR Pfam: PF01674; Lipase_2; 1.
SO SEQUENCE 290 AA; 30496 MW; D56B8508350F7432 CRC64;

Query Match 16.48; Score 178; DB 16; Length 290;
Best Local Similarity 28.68; Pred. No. 3.3e-06;
Matches 57; Conservative 30; Mismatches 62; Indels 50; Gaps 8;

OY 23 FAMQSAKAENHPVVMVHGIGAGSY-NFAGIKSYLVSGMSRGKLYAVDFMKTGTN- 79
DB 45 YTCAPS--AAHPRVVLHGFIDNRSVFLRLSLAONG--VFSLDGLGOLPGVLEF 99
OY 80 YNNGFV-----LSRFQVKVLEDFGAKKVDIVAHSMGANTPPYIKNDGKNKIENVVTL 133
DB 100 HGLSPVEKSAQGLAHNVKVLATGATGTTDLVGHGGMMPRYIKLFGAAEVVALGI 159
OY 134 GGANSTT-----SKALP-----GTPNQKILYTS 158
DB 160 APSNNGTTLGSLTRLLPFPGAEDLNEHTPALADQVVGSDVLTFLNAGGTPGVRTV 219
OY 159 IYSSADMIYNNYLSK-LDG 176
DB 220 LATKYDEVVTPYRGQFLDG 238

RESULT 8
O8RC83 PRELIMINARY; PRT; 403 AA.
ID O8RC83;
AC O8RC83;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Predicted acetyltransferases and hydrolases with the alpha/beta
DE hydrolase fold.
GN LIPA OR TRE0555.
OS Thermoaerobacter tengcongensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Thermoaerobacteriales; Thermoaerobacteriaceae; Thermoaerobacter.
OX NCBI_TaxID=119072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MB4T / JCM11007;
RX MEDLINE=21992816; PubMed=11997336;
RA Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
Tan H., Chen R., Wang J., Yu J., Yang H.;
RT "A complete sequence of T. tengcongensis genome.";
RL Genome Res. 12:689-700(2002).
DR EMBL: AE013025; AAM23831.1; -
KW Transferase; Hydrolase; Complete proteome.
SO SEQUENCE 403 AA; 45221 MW; DC31D5F86EC2CAC4 CRC64;

OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Brown S.P., Harris D.;
RL Submitted (Jul-2000) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (Jul-2000) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA MEDLINE-97000351; PubMed-8843436;
RA Redenbach M., Kieser H.M., Denapalate D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL Mol. Microbiol. 21:77-96(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinovich E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL: AL390188; CAB99145.1;
DR InterPro: IPR002918; Lipase_2.
DR InterPro: IPR000379; Ser-estrs-site.
DR Pfam: PF01674; Lipase_2; 1.
SQ SEQUENCE 289 AA; 31466 MW; 03D9002A2040FD52 CRC64;

Query Match 13.4%; Score 145.5; DB 16; Length 289;
Best Local Similarity 23.8%; Pred. No. 0.0012;
Matches 55; Conservative 35; Mismatches 76; Indels 65; Gaps 10;

QY 33 EH-NPVMVHG-IGGASYNFAGIKSYLVSGWSRGLYAVDFWDK-----TGTNNNG 83
DB 58 EHRPRVLVHGTFGRNGYTMNTAVPLLRHG--HVRFLDYGGHGNPLIFGLGDIKHA 114
QY 84 PVLSPFVQKVLDETGAKKVDIYAHSMGANTPYIYIKNLDGKNIENVVTLGGANSTSK 143
DB 115 RQLADFVEVLRTGAGQVDLVFGSGGMPRYLYNALGCGPKVHNFVGISPSNNGVTQ 174
QY 144 AL-----PGT-----DPNOKILYTSYSSA 163
DB 175 GLMNLARQIFGAVELLEGAAGEVVPWQLOHDLFOELADLGTTGCVRRITVATQY 234
QY 164 DMIVMNY-----LSKLDG--AKNAQIHGVG-----HIGLMSQV-NSLIR 201
DB 235 DDVVPYPTSCALAKTEGCVYNNIVLQDIDPDHPTVSMYNAVYLVNLEVK 285

RESULT 15
ID Q8YX63 PRELIMINARY; PRT; 211 AA.
AC Q8YX63;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hypothetical protein ALR1352.
GN ALR1352.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21595285; PubMed-11759840;
RA Kaneko T., Nakamura Y., Molk C.P., Kurita T., Sasamoto S.,
RA Watanabe A., Iriuch M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL: AP003585; BAB73309.1;
DR InterPro: IPR002047; AKH.
DR InterPro: IPR002918; Lipase_2.
DR InterPro: IPR000379; Ser-estrs-site.
DR Pfam: PF01674; Lipase_2; 1.
DR PROSITE: PS00256; AKH; UNKNOWN.1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 211 AA; 23718 MW; 08A8720935DA8F75 CRC64;

Query Match 13.3%; Score 145; DB 16; Length 211;
Best Local Similarity 26.5%; Pred. No. 0.00084;
Matches 54; Conservative 33; Mismatches 77; Indels 40; Gaps 8;

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DB 7 ORNPVLVHGHTDTEVFNPMAVYLRQLGMYTTLNLP-----NNGEAPLVNLAQ 57
QY 92 KYLDE-----TGAKKVDIYAHSMGANTPYIYIKNLDGKNIENVVTLGGANST--SK 143
DB 58 QVADYVCATITPEQPELDLVGFSWGGIVSRYYQKLGISRYQRFYISSLPHGQTVAVAS 117
QY 144 ALPG---TDPN-----OKILYTSYSSAD-MYMNYSKLDGAKNAQIHGV 185
DB 118 QHPCGYQMPNLSFLQDLNRDVQMLEQLNFTSIWTFYDLMIITPHSSKMPVGRKELTIPVA 177
QY 186 GHIGLIMN-----SQVNSLIRKGLN 205
DB 178 LHSWMLKDFRSIEVAVNALAEPIIN 201

Search completed: May 9, 2003, 16:21:56
Job time : 34 secs

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GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2003, 04:58:28 ; Search time 1429 Seconds
(without alignments)
13013.781 Million cell updates/sec

Title: US-09-905-666A-1

Perfect score: 639

Sequence: 1 atgaattgttaaagaag.....99ggccaataacgaattaa 639

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBankl:*
1: gb-ba:*
2: gb-hcg:*
3: gb-in:*
4: gb-om:*
5: gb-ov:*
6: gb-pat:*
7: gb-ph:*
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11: gb-sts:*
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33: em-htg-mus:*
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35: em-htg-rod:*
36: em-htg-mam:*
37: em-htg-vrt:*
38: em-sy:*
39: em-htgo-hum:*
40: em-htgo-mus:*
41: em-htgo-other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	639	100.0	639	6	AX418871 Sequence
2	629.4	98.5	639	6	AX418877 Sequence
3	627.8	98.2	639	6	AX418878 Sequence
4	626.2	98.0	639	6	AX365571 Sequence
5	626.2	98.0	639	6	AX418874 Sequence
6	626.2	98.0	639	6	AX418875 Sequence
7	623	97.5	639	6	AX418876 Sequence
8	606.4	94.9	639	6	AX418873 Sequence
9	573.4	89.7	35000	1	AB000617 Bacillus
10	573.4	89.7	221160	1	BSUB0002
11	571.8	89.5	1495	1	BACLP002
12	565.4	88.5	639	6	A02813
13	565.4	88.5	1831	6	A02815
14	565.4	88.5	1831	6	A02816
15	564.4	88.3	639	6	AX418872 Sequence
16	562.2	88.0	639	6	AX418879 Sequence
17	523.2	81.9	544	6	AX418894 Sequence
18	523.2	81.9	544	6	AX418923 Sequence
19	523.2	81.9	544	6	AX418924 Sequence
20	521.6	81.6	544	6	AX418913 Sequence
21	521.6	81.6	544	6	AX418916 Sequence
22	518.4	81.1	544	6	AX418896 Sequence
23	518.4	81.1	544	6	AX418915 Sequence
24	516.8	80.9	544	6	AX418910 Sequence
25	515.2	80.6	544	6	AX418904 Sequence
26	515.2	80.6	544	6	AX418914 Sequence
27	515.2	80.6	544	6	AX418922 Sequence
28	514.2	80.5	639	6	AX418886 Sequence
29	512.6	80.2	639	6	AX418885 Sequence
30	512	80.1	544	6	AX418903 Sequence
31	510.4	79.9	544	6	AX418893 Sequence
32	510.4	79.9	544	6	AX418900 Sequence
33	509.4	79.7	639	6	AX418884 Sequence
34	508.8	79.6	544	6	AX418912 Sequence
35	508.8	79.6	544	6	AX418919 Sequence
36	507.2	79.4	544	6	AX418891 Sequence
37	505.6	79.1	544	6	AX418892 Sequence
38	505.6	79.1	544	6	AX418898 Sequence
39	505.6	79.1	544	6	AX418901 Sequence
40	504	78.9	544	6	AX418897 Sequence
41	504	78.9	544	6	AX418920 Sequence
42	500.8	78.4	544	6	AX418921 Sequence
43	499.2	78.1	544	6	AX418899 Sequence
44	499.2	78.1	544	6	AX418918 Sequence
45	496	77.6	544	6	AX418902 Sequence

ALIGNMENTS

RESULT 1
AX418871
LOCUS
DEFINITION Sequence 1 from Patent WO0206457.
ACCESSION AX418871
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
1
Giver, L.J., Minshull, J. and Vogel, K.
Novel lipase genes
Patent: WO 0206457-A 1 24-JAN-2002;
Maxygen, Inc. (US)

Prod. No. is the number of results predicted by chance to have a

FEATURES	Location/Qualifiers
SOURCE	1. .639 /organism="Bacillus pumilus" /db_xref="taxon:1408"
BASE COUNT	201 a 123 c 159 g 156 t
ORIGIN	
Query Match	100.0%; Score 639; DB 6; Length 639;
Best Local Similarity	100.0%; Pred. No. 1,4e-184;
Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY 1	ATGAATTTGTAAGAGAGATCAATTCACATTTGGTGTCTACACCA 60
DB 1	ATGAATTTGTAAGAGAGATCAATTCACATTTGGTGTCTACACCA 60
OY 61	TGCGTGTTCGATCGACCGCGTACAAAGCGCTGAACACAAATCGATTATGTT 120
DB 61	TGCGTGTTCGATCGACCGCGTACAAAGCGCTGAACACAAATCGATTATGTT 120
OY 121	CACGGTATCGAGAGAGCTTACATATTTGGGGAATTAAGAGCTATCTGATCTCAG 180
DB 121	CACGGTATCGAGAGAGCTTACATATTTGGGGAATTAAGAGCTATCTGATCTCAG 180
OY 181	GGCTGTGTCACGGGCGCAACCTGTATCGCGTTATTTTGGGACAAACAGGACGAATAT 240
DB 181	GGCTGTGTCACGGGCGCAACCTGTATCGCGTTATTTTGGGACAAACAGGACGAATAT 240
OY 241	AACAATGGCCCGGTATTATACAGATTGTGTGCAAAAGTTTGTAGAGAAACGGGTGCGAAA 300
DB 241	AACAATGGCCCGGTATTATACAGATTGTGTGCAAAAGTTTGTAGAGAAACGGGTGCGAAA 300
OY 301	AAAGTGGATTTGTGCTCACAGTATGGGTGGCGGACACACCTTACTACTATAAAAT 360
DB 301	AAAGTGGATTTGTGCTCACAGTATGGGTGGCGGACACACCTTACTACTATAAAAT 360
OY 361	CTGGACGGCGGAATTAATTAAGTCTGTAACGCTTGGCGGCGCAACCGTTCTGACAG 420
DB 361	CTGGACGGCGGAATTAATTAAGTCTGTAACGCTTGGCGGCGCAACCGTTCTGACAG 420
OY 421	ACAACAGAGCGGCTTCCGGGAAACAGATCCAAATCAAAAGATTATTAACATCATCATTTAC 480
DB 421	ACAACAGAGCGGCTTCCGGGAAACAGATCCAAATCAAAAGATTATTAACATCATCATTTAC 480
OY 481	AGCAATGGCGAATGATTTGTCTATGAATTAATTAAGAGTGTAGAGGCTGTAAAGCGT 540
DB 481	AGCAATGGCGAATGATTTGTCTATGAATTAATTAAGAGTGTAGAGGCTGTAAAGCGT 540
OY 541	CAAAATTCATGGCGTGGGACATTTGTTATTTGATGAACAGGCAAGTCAACAGCGTGATT 600
DB 541	CAAAATTCATGGCGTGGGACATTTGTTATTTGATGAACAGGCAAGTCAACAGCGTGATT 600
OY 601	AAAGAAGAGCTGAACGGCGGGGCCCAAAATACGAATTAA 639
DB 601	AAAGAAGAGCTGAACGGCGGGGCCCAAAATACGAATTAA 639
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LOCUS	AX418877
DEFINITION	Sequence 7 from Patent WO0206457.
ACCESSION	AX418877
VERSION	AX418877.1 GI:21523732
KEYWORDS	
SOURCE	Bacillus firmus.
ORGANISM	Bacillus firmus.
REFERENCE	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
AUTHORS	1 Giver, L.J., Minshull, J. and Vogel, K.
TITLE	Novel lipase genes
JOURNAL	Patent: WO 0206457-A 7 24-JAN-2002;
FEATURES	Maxygen, Loc. (US)
SOURCE	1. .639 Location/Qualifiers

BASE COUNT		202	a	123	c	157	g	157	t	
ORIGIN										
Query Match		98.5%	Score 629.4;		DB 6;	Length 639;				
Best Local Similarity		99.1%;	Pred. No. 1.2e-181;							
Matches 633; Conservative		0;	Mismatches 6;		Indels	0;	Gaps	0;		
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Dg	1	ATGAATTTGTA	AAAAAGAGATCAT	TTGCAC	TGTGTA	ACAATTTTGTG	TCTGTCA	GTCACA	60	
Qy	61	TCGCGTTTGG	ATGTCACACCGCTG	ACA	AAAGCCGCTG	GAACACATCCAG	TGTTATG	GTT	120	
Dg	61	TCGCGTTTGG	ATGTCACACCGCTG	ACA	AAAGCCGCTG	GAACACATCCAG	TGTTATG	GTT	120	
Qy	121	CACGGTATCG	AGAGAGCTTCAT	TACAA	TTTGGGGAATTA	AGAGCTATCTG	TATCTCAG	180		
Dg	121	CACGGTATCG	AGAGAGCTTCAT	TACAA	TTTGGGGAATTA	AGAGCTATCTG	TATCTCAG	180		
Qy	181	GGCTGTACG	GGGGCAACCTG	TATGCGGTTG	ATTTTGGGCAAC	ACAGGGGCA	GAATTTAT	240		
Dg	181	GGCTGTGTAC	GGGGCAACCTG	TATGCGGTTG	ATTTTGGGCAAC	ACAGGGGCA	GAATTTAT	240		
Qy	241	AACAATGGC	CCGGTAATAT	CAAGATTTG	TGCAAAAAG	TTTTAGACG	AAACGGGTCG	GA	300	
Dg	241	AACAATGGC	CCGGTAATAT	CAAGATTTG	TGCAAAAAG	TTTTAGACG	AAACGGGTCG	GA	300	
Qy	301	AAAGGATAT	TGTCGTCACAGTAT	TGGGTGGCGG	GAACACACCTT	ACTACAT	TA	AAAAAT	360	
Dg	301	AAAGGATAT	TGTCGTCACAGTAT	TGGGTGGCGG	GAACACACCTT	ACTACAT	TA	AAAAAT	360	
Qy	361	CTGACGGC	GGAATTA	AAATTTG	AAAAACGTCG	TACGCTTGG	CGGGCGG	CAACCGTTG	CA	420
Dg	361	CTGACGGC	GGAATTA	AAATTTG	AAAAACGTCG	TACGCTTGG	CGGGCGG	CAACCGTTG	CA	420
Qy	421	ACAAAGCA	AGGGGCTTCCG	GAACAGATCC	CAATCA	AAAGATTTT	TATACACAT	CCATTTAC	480	
Dg	421	ACAAAGCA	AGGGGCTTCCG	GAACAGATCC	CAATCA	AAAGATTTT	TATACACAT	CCATTTAC	480	
Qy	481	AGCAGTGC	CGATATGAT	TGTCATG	AAATTA	ACTTATCA	AAATTA	AGACGTGCT	AAAAACGCT	540
Dg	481	AGCAGTGC	CGATATGAT	TGTCATG	AAATTA	ACTTATCA	AAATTA	AGACGTGCT	AAAAACGCT	540
Qy	541	CAATTCAT	TGCGCTTGG	GCACAT	TGCTTTAT	TGATGA	ACACGCAAGT	CAACAGCTG	ATT	600
Dg	541	CAATTCAT	TGCGCTTGG	GCACAT	TGCTTTAT	TGATGA	ACACGCAAGT	CAACAGCTG	ATT	600
Qy	601	AAAGAGAG	CACTGAACGG	CGGGCCCA	AAATTCAG	ATTTAA	639			
Dg	601	AAAGAGAG	CACTGAACGG	CGGGCCCA	AAATTCAG	ATTTAA	639			
RESULT 3										
LOCUS	AX418878	639 bp		DNA	linear		PAT 18-JUN-2002			
DEFINITION	Sequence 8 from Patent WO0206457.									
ACCESSION	AX418878									
VERSION	AX418878.1	GI:21523733								
KEYWORDS										
SOURCE	Bacillus badius.									
ORGANISM	Bacillus badius.									
REFERENCE	1. Giver, L.J., Minshull, J. and Vogel, K.									
AUTHORS	Novel lipase genes									
TITLE	Patent: WO 0206457-A 8 24-JAN-2002;									
JOURNAL	Maxygen, Inc. (US)									
FEATURES	Location/Qualifiers									
source	1..639									
/organism="Bacillus badius"										
/db_xref="taxon:1455"										

TITLE Novel Lipase genes
JOURNAL Patent: WO 0206457-A 4 24-JAN-2002;
Maxygen, Inc. (US)
FEATURES Location/Qualifiers
source 1..639
/organism="Bacillus lentus"
/db_xref="taxon:1467"

BASE COUNT 203 a 120 c 157 g 159 t
ORIGIN

Query Match 98.0%; Score 626.2; DB 6; Length 639;
Best Local Similarity 98.7%; Pred. No. 1.2e-180;
Matches 631: Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ATGAAATTTGTAAGAGAGATCATTCCTGTATACAAATTTGGTCTGCTACATCA 60
Db 1 ATGAAATTTGTAAGAGAGATCATTCCTGTATACAAATTTGGTCTGCTACATCA 60
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Db 121 CACGCTATCGAGAGAGCTTCATACAAATTTGGGGAATTAAGAGCTATCTGTATCTCAG 180
QY 181 GCGTGTACGCGGCGACGCTGTATGCGGTTGTTGGACAAAGAGGAGCAATTTAT 240
Db 181 GCGTGTACGCGGCGACGCTGTATGCGGTTGTTGGACAAAGAGGAGCAATTTAT 240
QY 241 AACATGCCCCGGTATTTATCAGATTTGTGCAAAAGTTTGAAGCAAGCGGTCGAAA 300
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Db 361 CTGACGCGGGAATTAATTAAGAAAGCTGTACGCTTGGGCGGCGCAACCGTTGACG 420
QY 421 ACAAGCAAGGCGCTCCGGAACAGATCAATCAAAAGATTTTATACATCCATTAC 480
Db 421 ACAAGCAAGGCGCTCCGGAACAGATCAATCAAAAGATTTTATACATCCATTAC 480
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RESULT 6
AX418875 639 bp DNA Linear PAT 18-JUN-2002
LOCUS AX418875
DEFINITION Sequence 5 from Patent WO0206457.
ACCESSION AX418875
VERSION AX418875.1 GI:21523730
KEYWORDS
SOURCE Bacillus circulans.
ORGANISM Bacillus circulans
REFERENCE 1
AUTHORS Giver, L.J., Minshull, J. and Vogel, K.
TITLE Novel Lipase genes
JOURNAL Patent: WO 0206457-A 5 24-JAN-2002;

Maxygen, Inc. (US)
FEATURES Location/Qualifiers
source 1..639
/organism="Bacillus circulans"
/db_xref="taxon:1397"

BASE COUNT 201 a 122 c 157 g 159 t
ORIGIN

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Best Local Similarity 98.7%; Pred. No. 1.2e-180;
Matches 631: Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ATGAAATTTGTAAGAGAGATCATTCCTGTATACAAATTTGGTCTGCTACATCA 60
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QY 601 AAAGAGAGCTGAACGCGGCGGCGCAAAATACGAATTA 639
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RESULT 7
AX418876 639 bp DNA Linear PAT 18-JUN-2002
LOCUS AX418876
DEFINITION Sequence 6 from Patent WO0206457.
ACCESSION AX418876
VERSION AX418876.1 GI:21523731
KEYWORDS
SOURCE Bacillus azotofornans.
ORGANISM Bacillus azotofornans
REFERENCE 1
AUTHORS Giver, L.J., Minshull, J. and Vogel, K.
TITLE Novel Lipase genes
JOURNAL Patent: WO 0206457-A 6 24-JAN-2002;
Maxygen, Inc. (US)
FEATURES Location/Qualifiers

Source	1..639	/organism="Bacillus azotoformans"
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ORIGIN		
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OY 61	TGCGTGTGGGATGCACCCGTCACAAAAGCCGCTGAACACAAATCCAGTTGTATGTT 120	
Db 61	TGCGTGTGGGATGCACCCGTCACAAAAGCCGCTGAACACAAATCCAGTTGTATGTT 120	
OY 121	CACGGTATCGAGAGAGCTTCATACAAATTTTGGGAAATTAAGAGCTATCTGTATCTGAG 180	
Db 121	CACGGTATCGAGAGAGCTTCATACAAATTTTGGGAAATTAAGAGCTATCTGTATCTGAG 180	
OY 181	GGCTGCTACGGGGGCAACCTGTATCCGTTGATTTTGGGACACAGAGGACGAATAT 240	
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Db 301	AAAGTGATATTTGTCGCTACAGATATGAGGTGGTGGCGGCAACACACTTACTACATAAAAT 360	
OY 361	CTGGACGGCGGAAATTAATTTGAAGAAACGTCGTAACGCTTGGGGGGCGGACCGTTCGACG 420	
Db 361	CTGGACGGCGGAAATTAATTTGAAGAAACGTCGTAACGCTTGGGGGGCGGACCGTTCGACG 420	
OY 421	ACAAGCAAGGCGCTTCCGGGAAACAGATCCAAATCAAAAGATTTTATACATCATCAATTAC 480	
Db 421	ACAAGCAAGGCGCTTCCGGGAAACAGATCCAAATCAAAAGATTTTATACATCATCAATTAC 480	
OY 481	AGCAGTGGCGATATGATGTGCATGAATTAATTAATAAATTAAGACGGGTCTAAAAACGCT 540	
Db 481	AGCAGTGGCGATATGATGTGCATGAATTAATTAATAAATTAAGACGGGTCTAAAAACGCT 540	
OY 541	CAAAATTCATGGCGTTGGGCACATTGGTTATTTGATGAAGACAGCAAGTCAACAGCCTGATT 600	
Db 541	CAAAATTCATGGCGTTGGGCACATTGGTTATTTGATGAAGACAGCAAGTCAACAGCCTGATT 600	
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Db 601	AAAGAAAGACTGAACGGCGGGGCCCTAGATACAAATTA 639	
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LOCUS	AX418873	
DEFINITION	Sequence 3 from Patent WO0206457.	
ACCESSION	AX418873	
VERSION	AX418873.1	
KEYWORDS	GI:21532728	
SOURCE		
ORGANISM	Bacillus megaterium.	
REFERENCE	Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.	
AUTHORS	Glover, L.J., Minshull, J. and Vogel, K.	
TITLE	Novel lipase genes	
JOURNAL	Patent: WO 0206457-A 3 24-JAN-2002;	
FEATURES	Maxygen, Inc. (US)	
source	Location/Qualifiers	
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Db	61	TCGGTGTTCGATG	CAGACCCGTCAGCAAAACCCGTCG	119	
QY	121	CAC-GGTATCGGAGAG	AGCTTCATACAAATTTTGGGGAATTAAGAGCTATCTGTATCTCA	179	
Db	120	CACGTGTATCCGAGAG	AGCTTCATACAAATTTTGGGGAATTAAGAGCTATCTGTATCTCA	179	
QY	180	GGGTGGTCACGGGGCA	AGCTGTATGCGGTGATTTTGGGCAAGACAGGAGCAATTA	239	
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QY	360	TCGTGGACGGCGGAAT	ATAAATTTGAAAAAGCTGTACGCTTGGCGGCGGAACACTTACTACATATAAAA	419	
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QY	420	GACAAGCAGGCGCTT	CGGAGACAGATCCAAATCAAAAGATTTTATACATCCATTTA	479	
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QY	480	CAGAGAGCCGATTTG	ATTCATGAATTTACTTATCAAAATAGACGGTGGCAAAAAGCG	539	
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Db	540	TCAATTCATGCGCTT	GGGCACATTTGTTATGTATGAACACCGCAAGTCAAGCGCTGAT	599	
QY	600	TAAAGAAGGACTGAA	AGCGGGGCGCAAAATACGATTA	639	
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LOCUS	AB000617				
DEFINITION	Bacillus subtilis genomic DNA, 22 to 25 degree region, complete cds.				
ACCESSION	AB000617				
VERSION	AB000617.1 GI:2415716				
KEYWORDS	Ycck; NaB; yceG; yceK; yceJ; yceI; yceH; yceF; yceE; yceD; yceC; yceB; yceA; ycdI; ycdH; ycdG; ycdF; RapD; ycdB; ycdA; ycdA; yceH; yccG; yccF; yccE; yccc; yccb; Tricycylglycerol lipase; LmrA; yceA; LmrB; ycdU.				
SOURCE	Bacillus subtilis (strain:168 trpC2) DNA.				
ORGANISM	Bacillus subtilis				
REFERENCE	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.				
AUTHORS	1 (sites)				
TITLE	Kumano,M., Tamakoshi,A. and Yamane,K. A 32 kb nucleotide sequence from the region of the lincomycin-resistance gene (22-25 degree) of the Bacillus subtilis chromosome and identification of the site of the lin-2 mutation				
JOURNAL	Unpublished				

REFERENCE 2 (bases 1 to 35000)
AUTHORS Yamane,K.
TITLE Direct Submission
JOURNAL Submitted (20-JUN-1997) Kunio Yamane, University of Tsukuba,
Institute of Biological Sciences: 1-1-1 Ten-ohda, Tsukuba, Ibaraki
305, Japan (Tel:0298-53-6680, Fax:0298-53-6680)
Location/Qualifiers
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Best Local Similarity 93.6%; Pred. No. 3.8e-164;
Matches 598; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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DB 5838 CAAATTCATGCGCTGGGACATGCGCTTCTGACGACGCAACGACGCTGAT 5897
OY 601 AAAGAAGCATGACGCGCGGCGCAAAATACGATTA 639
DB 5898 AAAGAAGCATGACGCGCGGCGCAAAATACGATTA 5936

RESULT 10
BSUB0002
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

1 (bases 1 to 221160)
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
Bacillus subtilis.
Bacillus subtilis complete genome (section 2 of 21): from 194651 to
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299105 AL009126
299105.1 GI:2632457

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FEATURES

source

TITLE

The complete genome sequence of the gram-positive bacterium

Bacillus subtilis

Nature 390 (6657), 249-256 (1997)

98044033

9384377

2 (bases 1 to 221160)

Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A.

Direct Submission

Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pasteur,

Regulation de l'Expression Genetique, 28 rue du Docteur Roux, 75724

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adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45

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Query Match 89.7%: Score 573.4; DB 1; Length 221160;
Best Local Similarity 93.6%; Pred. No. 5,3e-164;
Matches 598; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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Oy 61 TCGCTGTTGGCATCGACCGCTCAGCAAAAGCCGCTGAACACATCCAGTTTATGCTT 120
Db 97169 TCGCTGTTGGCATCGACCGCTCAGCAAAAGCCGCTGAACACATCCAGTTTATGCTT 97228
Oy 121 CACGATATCGAGAGCTTCATACATTTTGGGGAATTAAGAGCTATCTGATCTCAG 180
Db 97229 CACGATATCGAGAGGATCATTCATTTTGGGGAATTAAGAGCTATCTGATCTCAG 97288
Oy 181 GCGTGTACAGGGGCAAGCTGTATCGGTTGATTTTGGGACAGACAGGAGCAATTAAT 240
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RESULT 11
LOCUS BACLIPASE 1495 bp DNA linear ECT 26-APR-1993
DEFINITION Bacillus subtilis lipase (lipo) gene, complete cds.
ACCESSION M74010
VERSION M74010.1 GI:143153
KEYWORDS lipo gene; lipase.
SOURCE Bacillus subtilis (strain W168) DNA.
ORGANISM Bacillus subtilis
REFERENCE 1 (bases 1 to 1495)
AUTHORS Dartois V., Baulard A., Schanck K. and Colson C.
TITLE Cloning, nucleotide sequence and expression in Escherichia coli of
a lipase gene from Bacillus subtilis 168
JOURNAL Biochim Biophys. Acta 1131 (3), 253-260 (1992)
MEDLINE 93329538
PUBMED 1320940
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BASE COUNT 459 a 307 c 344 g 385 t
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Best Local Similarity 97.4% Pred. No. 6.5e-164;
Matches 597; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
Oy 1 ATGAATTTGTAAAGAAGATCATTCACCTTGTAAACATTTTGTGCTGTCACTACA 60
Db 478 ATGAATTTGTAAAGAAGATCATTCACCTTGTAAACATTTTGTGCTGTCACTACA 537
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Oy 181 GCGTGTACAGGGGCAAGCTGTATCGGTTGATTTTGGGACAGACAGCAATTAAT 240
Db 658 GCGTGTACAGGGGCAAGCTGTATCGGTTGATTTTGGGACAGACAGCAATTAAT 717
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Db 718 AACATGACCGGCTATATACAGATTTTGCAGAAAGGTTTACAGCAAGGGGTGCAAA 777
Oy 301 AAAGTGATATTTGCTCAGATATGAGTGGGCGGCAACACCTTACTACTATAAAAT 360
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Oy 361 CTGACGGCGGCAATTAATTAAGAAACGTCGTACGCTTGGCGGCGCAACCGTTGACG 420
Db 838 CTGACGGCGGCAATTAATTAAGAAACGTCGTACGCTTGGCGGCGCAACCGTTGACG 897
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Oy 481 AGCAGTCCGCAATGATGTGATGATTAATTAATTAAGAAAGGTTGCTTAAAGAGCT 540
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Oy 601 AAAGAGGAGCTGAACGGGCGGCGCAAAATACGAATTA 639
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RESULT 12
LOCUS A02813 639 bp DNA linear PAT 16-JUN-1993
DEFINITION G.candidum gene for lipase.

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ACCESSION	A02813
VERSION	A02813.1
KEYWORDS	GI:410743
SOURCE	Iipase.
ORGANISM	Galeatcomyces geotrichum. Galeatcomyces geotrichum Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales; Dipodascaceae; Galeatcomyces.
REFERENCE	Vandamme, E., Schanck-Brodbeck, K.H., Colson, C. and Hanotier, J.D.V. DNA segment coding for a specific Iipase, vectors for the expression thereof, microorganisms transformed by these vectors and use of these microorganisms for the production of the Iipase Patent: EP 0243338-A 1 28-OCT-1987;
AUTHORS	FINA RESEARCH S.A
TITLE	
JOURNAL	
FEATURES	
source	Location/Qualifiers 1..639 /organism="Galeatcomyces geotrichum" /db_xref="taxon:27317"
CDS	1..639 /codon_start=1 /product="Iipase" /protein_id="CAA00273.1" /db_xref="GI:410744"
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Matches 593:	Conservative 0; Mismatches 46; Indels 0; Gaps 0;
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Db	121 CACGCTATCGAGAGAGCACTTCAATTTTTCGGGAATTAAGAGCTATCCCTATCTGAG 180
QY	181 GGCTGCTACGGGGCAGACTGTATGCCGTTATTTTGGACACAGACAGGACGATATAT 240
Db	181 GGCTGCTACGGGGCAGACTGTATGCCGTTATTTTGGACAGACAGGACGACAAATATAT 240
QY	241 AACATGGCCGGATTTATTCAGATTTGTGCAAAAAGTTTAGACGAAGGCGGCGGAAA 300
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QY	301 AAAGTGAATTTGTGCTCACAGTATGGGTGGCGGAGACACACTTACTACATATAAAAT 360
Db	301 AAAGTGAATTTGTGCTGCGCAGCATGGGGGGCGGAGACACACTTACTACATATAAAAT 360
QY	361 CTGAGCGCGCGGAATTAATTTGAANAAGCTGTAACGCTTGGCGGCGGCAACCGTTGCAGC 420
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QY	421 ACAAGCAGAGGGCTTCCGGGAACAGATCCAATCAAAAGATTTTATPACATCCATTAC 480
Db	421 ACAGGCAAGGGCTTCCGGGAACAGATCCAATCAAAAGATTTTATPACATCCATTAC 480
QY	481 AGCAGTCCGATATGATTTGTCATGAATTAATTACAAATTAAGATGAGTGAANAAGCTT 540
Db	481 AGCAGTCCGATATGATTTGTCATGAATTAATTACAAATTAAGATGAGTGAANAAGCTT 540
QY	541 CAATATCATGGCGTTGGGACATTTGTTATTTGATGACACGCAAGTCAACGCTGATT 600
Db	541 CAATATCATGGCGTTGGGACATTTGTTGATGACACGCAAGTCAACGCTGATT 600

LOCUS	LOCUS	1831 bp	DNA	linear	PAT 16-JUN-1993
LOCUS	A02815	1831 bp	DNA	linear	PAT 16-JUN-1993
DEFINITION	Artificial gene for lipase comprising HindIII-EcoRI segment.				
ACCESSION	A02815				
VERSION	A02815.1	GI:412317			
KEYWORDS	lipase.				
SOURCE	synthetic construct.				
ORGANISM	synthetic construct.				
REFERENCE	artificial sequences.				
AUTHORS	1 (bases 1 to 1831)				
TITLE	Vandamme,E., Schanck-Brodbeck,K.H., Colson,C. and Hanotier,J.D.V.				
JOURNAL	DNA segment coding for a specific lipase, vectors for the				
FEATURES	expression thereof, microorganisms transformed by these vectors and				
source	use of these microorganisms for the production of the lipase				
	Patent: EP 0243338-A 3 28-Oct-1987;				
	FINA RESEARCH S.A				
	Location/Qualifiers				
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	165..170				
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	SSADMIYMNLSRLDGARVNOIGHVGIGLILYSSVNSLITKEGGGONTN"				
BASE COUNT	585 a 367 c 416 g 463 t				
ORIGIN					
Query Match	88.5%: Score 565.4; DB 6; Length 1831;				
Best Local Similarity	92.8%: Pred. No. 6.2e-162;				
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263	TGCGTGTGGATGACACCCCTCAGCAAAAGCCGCTGAAACAAATCCAGTTGATG	322			
121	CACGTTATCGAGAGAGCTTACATATTTGGGGAAATTAAGAGCTATCTGATCTCAG	180			
323	CACGTTATCGAGAGAGAGCTTACATATTTGGGGAAATTAAGAGCTATCTGATCTCAG	382			
181	GGCTGTCACGGGGCAACCTGATGCGGTGATTTTGGACAAGACAGGAGCAATAT	240			
383	GGCTGTCACGGGGCAACCTGATGCGGTGATTTTGGACAAGACAGGAGCAATAT	442			
241	AACATGACCCGCTTATATCAGATTTGCAAAAAGCTTTTGAAGAGAAACGGTGC	300			
443	AACATGACCCGCTTATATCAGATTTGCAAAAAGCTTTTGAAGAGAAACGGTGC	502			
301	AAAGTGAATTTGCTCAGATGATGGGTGGCGGACACACACCTTACTACATAAAAT	360			
503	AAAGTGAATTTGCTCAGATGATGGGTGGCGGACACACACCTTACTACATAAAAT	562			
361	CTGAGCGCGGAAATTAATGAAGAAAGCTGTAACGCTGGCGGCGGACCGTTG	420			
563	CTGAGCGCGGAAATTAATGAAGAAAGCTGTAACGCTGGCGGCGGACCGTTG	622			

QY	421	ACAACGAGGCGCTTCGCGGAACACATCCAAATCAAAAGATTTTATACACATCCATTAC	480
Db	623	ACAGGCAAGGCGCTTCGCGGAACACATCCAAATCAAAAGATTTTATACACATCCATTAC	682
QY	481	ACCACTGCCGATATATGTGTCATGAATTACTATCAAAATTAAGACGCTGCTAAAGCCT	540
Db	683	ACCACTGCCGATATATGTGTCATGAATTACTATCAAAATTAAGATGTGCTGTAAGAACGTT	742
QY	541	CAAAATTCATGGCGTTGGGCACATGTGTTTATGTATGAACAGCCAAAGTCACAGCCTGATT	600
Db	743	CAAAATTCATGGCGTTGGGCACATGTGTTTATGTATGAACAGCCAAAGTCACAGCCTGATT	802
QY	601	AAAGAAGCACTGAACGGCGGGCGCAAAATACGATTAA	639
Db	803	AAAGAAGGCGTGAACGGCGGGGCCAAGATTCGAAATTA	841
RESULT 14			
LOCUS	A02816/c	A02816	
DEFINITION	Artificial sequence comprising HindIII-EcoRI segment, reverse complement.	1831 bp	DNA
ACCESSION	A02816		
VERSION	A02816.1		
KEYWORDS	GI:410908		
SOURCE	synthetic construct.		
ORGANISM	synthetic construct.		
REFERENCE	1 (bases 1 to 1831)		
AUTHORS	Vandamme, E., Schanck-Brodbeck, K.H., Colson, C. and Hanotier, J.D.V.		
TITLE	DNA segment coding for a specific lipase, vectors for the expression thereof, microorganisms transformed by these vectors and use of these microorganisms for the production of the lipase		
JOURNAL	Patent: EP 0243338-A 4 28-Oct-1987;		
FINA RESEARCH S.A			
FEATURES	Location/Qualifiers		
source	1..1831		
BASE COUNT	463 a 416 c 367 g 585 t		
ORIGIN	1		
Query Match	88.5%; Score 565.4; DB 6; Length 1831;		
Best Local Similarity	92.8%; Pred. No. 6.2e-162;		
Matches 593; Conservative 0; Mismatches 46; Indels 0; Gaps 0;			
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QY	61	TGCGTGTTCGATCGACCGCTGACAAAAGCCGCTGAACACATCCAGTTTATGCTT	120
Db	1569	TGCGTGTTCGCTTCACCCGTCACAAAAGCCGCTGAACACAAATCCAGTGTATGCTT	1510
QY	121	CACGTTATCGAGAGCTTCATACATTTTGGGGAATTAAGACTATCTGATCTAG	180
Db	1509	CACGTTATCGAGAGGCGACACATTCATTTTGGGGAATTAAGAGCTATCCGATCTAG	1450
QY	181	GGCTGTGTCAGGGGCAACCTGTATCGGTTGATTTTGGGACACAGACGAGCAATTA	240
Db	1449	GGCTGTGTCAGGGGCAACCTGTATCGAGTTGATTTTGGGACACAGCAAAATTA	1390
QY	241	AACATTTGCCCGCTTTTATCAACGATTTTGCAAAAAGTTTATAGACAAAGGTCGAA	300
Db	1389	AACATTTGCCGCTTTTATCAACGATTTTGCAAAAAGTTTATAGATGAACGCTGCGAA	1330
QY	301	AAAGTGATATTTGTCGTACAGTATGGGTGGCGGACACACCTTACTATCAATAAAAT	360
Db	1329	AAAGTGATATTTGTCGTACAGTATGGGTGGCGGACACACCTTACTATCAATAAAAT	1270
QY	361	CTGAGCGCGCAATTAATTAAGTCTGTAACGCTTGGCGCGCAACGTTGACG	420

Dd	1269	CTGGACGGGCGGAATAAAGTTGCCAAACGTGCGAGCCTTGGGGGCGCAACCGTTTGACG	1210
Qy	421	ACAACAGAAGCCCTTCGGGAACAGATCCAATCAAAGATTATTAACATCCATTATAC	480
Dd	1209	ACAGGCAGAGGCGCTTCGGGAACAGATCCAATCAAAGATTATTAACATCCATTATAC	1150
Qy	481	AGCATGTCCGATATATTGTGTCATGAATTACTATCAAAATTAAGACGGGTCAAAAAAGCT	540
Dd	1149	AGCATGTCCGATATATTGTGTCATGAATTACTATCAAAATTAAGACGGGTCAAAAAAGCT	1090
Qy	541	CAAAATTCATGGCGGTGGGCACATTGGTTATVTGATGAACAGCCCAAGTCACAGCCCTGATT	600
Dd	1089	CAAAATTCATGGCGGTGGGCACATCGCCCTTCGTGTACACAGCCCAAGTCACAGCCCTGATT	1030
Qy	601	AAGAAGACACTGAACGGCGGGGCCAAAATACGAATTTAA	639
Dd	1029	AAGAAGAGGCGTAGAACGGCGGGGCCAAGATTCGAATTTAA	991
RESULT	15		
LOCUS	AX418872	639 bp	DNA Linear PAT 18-JUN-2002
DEFINITION	Sequence 2 from Patent WO0206457.		
ACCESSION	AX418872		
VERSION	AX418872.1 GI:21523727		
KEYWORDS	Bacillus subtilis.		
SOURCE	Bacillus subtilis.		
ORGANISM	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
REFERENCE	1 Giver, L.J., Minshull, J. and Vogel, K.		
AUTHORS	Novel lipase genes		
TITLE	Patent: WO 0206457-A 2 24 -JAN-2002;		
JOURNAL	Maxygen, Inc. (US)		
FEATURES	Location/Qualifiers		
Source	1..639 /organism="Bacillus subtilis"		
BASE COUNT	194 a 126 c 161 g 158 t		
ORIGIN	/db_xref="taxon:1423"		
Query Match	88.3%; Score 564.4; DB 6; Length 639;		
Best Local Similarity	92.8%; Pred. No. 1e-161;		
Matches	592; Conservative 0; Mismatches 46; Indels 0; Gaps 0;		
Qy	1	ATGAATTTGTAAAGAAGATCATTCACATTGCTGAACATTTTGTGCTGCAGTCACA	60
Dd	1	ATGAATTTGTAAAGAAGATCATTCACATTGCTGAACATTTTGTGCTGCAGTCACA	60
Qy	61	TGCGTGTTCGAGTCAGCCGTCAGCAAAAGCCGCTGAACACATTCAGTTTATGTT	120
Dd	61	TGCGTGTTCGAGTCAGCCGTCAGCAAAAGCCGCTGAACACATTCAGTTTATGTT	120
Qy	121	CACGGTATCGGAGGAGCTCATACAAATTTGGGGAAATTAAGAGCTATCTGTATTCAG	180
Dd	121	CACGGTATTCGAGGAGGAGCTCATACAAATTTGGGGAAATTAAGAGCTATCTGTATTCAG	180
Qy	181	GCGTGTACGCGGAGCACTGTATGCGGTTGATTTTTTGGCAAGACAGGAGCAGATTAT	240
Dd	181	GCGTGTGCGCGGAGCAACCTGTATGCTGATTTTTTGGCAAGACAGCACAATTTAT	240
Qy	241	AACATATGCCCCGGTATTATCACAGATTGTGCAAAAAGTTTATAGACAAACGGGTCCGAA	300
Dd	241	AACATATGACCGATVATACACAGATTGTGCAAAAAGTTTATAGATGAACGGGTCCGAA	300
Qy	301	AAAGTGATATTGTTCGTACAGTATGGGTGGCGGAGACACACCCTTACTATCAATAAAAT	360
Dd	301	AAAGTGATATTGTTCGTACACAGATGGGGGCGGGAACACACTTTACTATCAATAAAAT	360
Qy	361	CTGGACGGCGGAATAAATTTGAAAGCTGTAACGCTTGGCGGGCGGAACGTTTCGACG	420
Dd	361	CTGGACGGCGGAATAAATTTGAAAGCTGTAACGCTTGGCGGGCGGAACGTTTTCGACG	420

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Page 12

QY	421	ACAAAGCAGGGCGCTTCCGGGAAACAGATCCAAATCAAAAAGATTTATACATCATCATTTAC	480
Db	421	ACAGGCAAGGGCGCTTCCGGGAAACAGATCCAAATCAAAAAGATTTATACATCATCATTTAC	480
QY	481	AGCAGTGGCGGATGATGTTGTCATGAATTTACTTATCAAAATTTAGACGGTGTAAAAACGCT	540
Db	481	AGCAGTGGCGGATGATGTTGTCATGAATTTACTTATCAAAATTTAGACGGTGTAAAAACGCT	540
QY	541	CAAAATTCATGGCGCTTTGGGACACATTTGGTTTATTGATGAAACGCCAAGTCACACGCTGATT	600
Db	541	CAAAATTCATGGCGCTTTGGGACACATTTGGCGCTTTCTGTACAGCAGGCCAAGTCACACGCTGATT	600
QY	601	AAAGAGAGCTGTAACGGCGGGGGGCAAAATTCAGAAATTA	638
Db	601	AAAGAGAGCTGTAACGGCGGGGGGCAAAATTCAGAAATTA	638

Search completed: May 18, 2003, 07:31:31
Job time : 1547 secs

QY 181 GGCTGTCACGGGCAAGCTGTATCGGTTGATTTTGGGACAGACAGCAATTTAT 240
DB 181 GGCTGTCACGGGCAAGCTGTATCGGTTGATTTTGGGACAGACAGCAATTTAT 240
QY 241 AACAAATGCGCGGTATATACAGATTTTGTCAAAGGTTTATAGAGAAACGGGTCGAAA 300
DB 241 AACAAATGCGCGGTATATACAGATTTTGTCAAAGGTTTATAGAGAAACGGGTCGAAA 300
QY 301 AAAGTGATTTGTGCTACAGATTTGCTGCGGCAACGCTTACATCAATTTAAAT 360
DB 301 AAAGTGATTTGTGCTACAGATTTGCTGCGGCAACGCTTACATCAATTTAAAT 360
QY 361 CTGACGCGGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
DB 361 CTGACGCGGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
QY 421 ACAAGCAAGGCGCTTCGCGGCAACAGATCCAAATCAAAAGATTTATACATTCATTTAC 480
DB 421 ACAAGCAAGGCGCTTCGCGGCAACAGATCCAAATCAAAAGATTTATACATTCATTTAC 480
QY 481 AGCAGTGGCGATATGATTTGCTCAATTAATTAATTAATTAATTAATTAATTAAT 540
DB 481 AGCAGTGGCGATATGATTTGCTCAATTAATTAATTAATTAATTAATTAATTAAT 540
QY 541 CAAATTCATGCGGTGCGGCAATTTGATTAATTAATTAATTAATTAATTAATTAAT 600
DB 541 CAAATTCATGCGGTGCGGCAATTTGATTAATTAATTAATTAATTAATTAATTAAT 600
QY 601 AAAGAAGAGCTGTAACGGGCGGCAATTAATTAATTAATTAATTAATTAATTAAT 639
DB 601 AAAGAAGAGCTGTAACGGGCGGCAATTAATTAATTAATTAATTAATTAATTAAT 639

RESULT 3

ABK33826
ID ABK33826 standard; DNA; 639 BP.

XX AC ABK33826;

XX DT 08-MAY-2002 (first entry)

XX DE Bacillus lipase polynucleotide #8.

XX KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
KW human foodstuff; cheese; food emulsifier; leather tanning; gene; ds;
KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
KW gastrointestinal.

XX KW Bacillus badius.

XX OS WO200206457-A2.

XX PN 24-JAN-2002.

XX PD 13-JUL-2001; 2001WO-US22160.

XX PF 13-JUL-2000; 2000US-217954P.

XX PR 21-JUN-2001; 2001US-300378P.

XX PA (MAXY-) MAXYGEN INC.

XX PI Gliver LJ, Minshull J, Vogel K;

XX DR WPI: 2002-171805/22.

XX P-PSDB: AA083848.

XX Nucleic acids encoding lipase enzymes which are useful as supplements
PT in animal feeds, as agents of flavour modification and for treating
PT Crohn's disease and coeliac disease -

PS Claim 81: Page 120; 196pp; English.

CC The invention relates to new Bacillus lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences ABK33819-ABK33874 represent Bacillus lipase
CC polynucleotides of the invention.

XX Sequence 639 BP; 202 A; 122 C; 157 G; 158 T; 0 other;

QY Query Match 98.2%; Score 627.8; DB 24; Length 639;

DB Best Local Similarity: 98.9%; Pred. No. 1.4e-186;

Matches 632; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGAATTTGTAAAAAGAGATCATTTGCGGCAATTTAGAGCTATCTGATCTGACA 60

DB 1 ATGAATTTGTAAAAAGAGATCATTTGCGGCAATTTAGAGCTATCTGATCTGACA 60

QY 61 TCGCTGTTGGCATGACGCGCTGACAAAGCGCGTGAACACATTCAGTTTATGTT 120

DB 61 TCGCTGTTGGCATGACGCGCTGACAAAGCGCGTGAACACATTCAGTTTATGTT 120

QY 121 CACGGTATCGAGGAGGCTTCATATCAATTTGCGGCAATTTAGAGCTATCTGATCTGACA 180

DB 121 CACGGTATCGAGGAGGCTTCATATCAATTTGCGGCAATTTAGAGCTATCTGATCTGACA 180

QY 181 GGCTGTCACGGGCAAGCTGTATCGGTTGATTTTGGGACAGACAGCAATTTAT 240

DB 181 GGCTGTCACGGGCAAGCTGTATCGGTTGATTTTGGGACAGACAGCAATTTAT 240

QY 241 AACAAATGCGCGGTATATACAGATTTTGTCAAAGGTTTATAGAGAAACGGGTCGAAA 300

DB 241 AACAAATGCGCGGTATATACAGATTTTGTCAAAGGTTTATAGAGAAACGGGTCGAAA 300

QY 301 AAAGTGATTTGTGCTACAGATTTGCTGCGGCAACGCTTACATCAATTTAAAT 360

DB 301 AAAGTGATTTGTGCTACAGATTTGCTGCGGCAACGCTTACATCAATTTAAAT 360

QY 361 CTGACGCGGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420

DB 361 CTGACGCGGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420

QY 421 ACAAGCAAGGCGCTTCGCGGCAACAGATCCAAATCAAAAGATTTATACATTCATTTAC 480

DB 421 ACAAGCAAGGCGCTTCGCGGCAACAGATCCAAATCAAAAGATTTATACATTCATTTAC 480

QY 481 AGCAGTGGCGATATGATTTGCTCAATTAATTAATTAATTAATTAATTAATTAAT 540

DB 481 AGCAGTGGCGATATGATTTGCTCAATTAATTAATTAATTAATTAATTAATTAAT 540

QY 541 CAAATTCATGCGGTGCGGCAATTTGATTAATTAATTAATTAATTAATTAATTAAT 600

DB 541 CAAATTCATGCGGTGCGGCAATTTGATTAATTAATTAATTAATTAATTAATTAAT 600

QY 601 AAAGAAGAGCTGTAACGGGCGGCAATTAATTAATTAATTAATTAATTAATTAAT 639

DB 601 AAAGAAGAGCTGTAACGGGCGGCAATTAATTAATTAATTAATTAATTAATTAAT 639

RESULT 4

ABK33822
ID ABK33822 standard; DNA; 639 BP.

XX AC ABK33822;

DT 08-MAY-2002 (first entry)
 XX
 DE Bacillus lipase polynucleotide #4.
 XX
 KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
 KW human foodstuff; cheese; food emulsifier; leather tanning; gene; ds;
 KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
 KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
 KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
 KM gastrointestinal.
 XX
 OS Bacillus lentus.
 XX
 PN W0200206457-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 13-JUL-2001; 2001WO-US22160.
 XX
 PR 13-JUL-2000; 2000US-217954P.
 PR 21-JUN-2001; 2001US-300378P.
 XX
 PA (MAXY-) MAXYGEN INC.
 XX
 PI Giver LJ, Minshull J, Vogel K;
 XX
 DR WPI; 2002-171805/22.
 DR P-PSDB; AAU83844.
 XX
 PT Nucleic acids encoding lipase enzymes which are useful as supplements
 PT in animal feeds, as agents of flavour modification and for treating
 PT Crohn's disease and coeliac disease -
 XX
 PS Claim 81; Page 118; 196pp; English.
 XX
 CC The invention relates to new Bacillus lipase enzymes and the nucleic
 CC acids encoding them. The lipase polypeptides are useful as supplements in
 CC animal feeds, as agents of flavour modification and fat modification in
 CC human foodstuffs (e.g. cheese), as agents in the creation of food
 CC emulsifiers, as agents for tanning/processing of leather and as cleaning
 CC agents. They are also useful for treating Crohn's disease, cystic
 CC fibrosis, coeliac disease, indigestion, obesity and other
 CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
 CC conditions can be therapeutically or prophylactically treated via a
 CC method of hydrolysing a lipid comprising expressing in a target cell or
 CC contacting a target cell with an effective amount of DNA or protein of
 CC the invention. Sequences ABK33819-ABK33874 represent Bacillus lipase
 CC polynucleotides of the invention.
 CC
 XX
 SQ Sequence 639 BP; 203 A; 120 C; 157 G; 159 T; 0 other;
 Query Match 98.0%; Score 626.2; DB 24; Length 639;
 Best Local Similarity 98.7%; Pred. No. 4.3e-186;
 Matches 631; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 1 ATGAAATTTGTAAGAGAGATCATTCGACTGTGTAACAAATTTGGTCTGCTCACTCA 60
 DB 1 ATGAAATTTGTAAGAGAGATCATTCGACTGTGTAACAAATTTGGTCTGCTCACTCA 60
 QY 1 TCGGTGTTGGATGACGCGTCGACAAAGCCGCTGAACCAATCCGTTGTTATGTT 120
 DB 1 TCGGTGTTGGATGACGCGTCGACAAAGCCGCTGAACCAATCCGTTGTTATGTT 120
 QY 121 CACGATATCGAGAGAGCTTATACAAATTTTCGGGAATTAAGAGCTATCTGATCTCAG 180
 DB 121 CACGATATCGAGAGAGCTTATACAAATTTTCGGGAATTAAGAGCTATCTGATCTCAG 180
 QY 121 CAGGATATCGAGAGAGCTTATACAAATTTTCGGGAATTAAGAGCTATCTGATCTCAG 180
 DB 121 CAGGATATCGAGAGAGCTTATACAAATTTTCGGGAATTAAGAGCTATCTGATCTCAG 180
 QY 181 GGTGTGTCAGGCGGACGCTATGCGGTGATTTTGGCAACAGACGGAGCAATAT 240
 DB 181 GGTGTGTCAGGCGGACGCTATGCGGTGATTTTGGCAACAGACGGAGCAATAT 240
 QY 241 AACATGCGCGGATATTCAGATTTGTGCAAAAGTTTACGAAAGCGGTGCGGAA 300
 DB 241 AACATGCGCGGATATTCAGATTTGTGCAAAAGTTTACGAAAGCGGTGCGGAA 300

DB 241 AACATGCGCGGATATTCAGATTTGTGCAAAAGTTTACGAAAGCGGTGCGGAA 300
 QY 301 AAGTGTATTTGTCGCTACAGATATGAGTGCGCGGACACACACTTACTACATAAAAAAT 360
 DB 301 AAGTGTATTTGTCGCTACAGATATGAGTGCGCGGACACACACTTACTACATAAAAAAT 360
 QY 361 CTGAGCGCGGAAATTAATTAAGAAACGTCGTACGCTTGCGGCGGACCGTTGACG 420
 DB 361 CTGAGCGCGGAAATTAATTAAGAAACGTCGTACGCTTGCGGCGGACCGTTGACG 420
 QY 421 ACAAGCAAGCGGCTCCGCGGACAGATCCAAATCAAAAGTTTATACATCCATTCAC 480
 DB 421 ACAAGCAAGCGGCTCCGCGGACAGATCCAAATCAAAAGTTTATACATCCATTCAC 480
 QY 481 AGCAGTCCGATATGATTTGTCATGAATTAATTAAGAAATTAAGAGCGTGAACAGCT 540
 DB 481 AGCAGTCCGATATGATTTGTCATGAATTAATTAAGAAATTAAGAGCGTGAACAGCT 540
 QY 541 CAAATTCATGCGGCTTGCGGACATTTGTTATGATGAACAGCCAAAGTCACAGCTGATT 600
 DB 541 CAAATTCATGCGGCTTGCGGACATTTGTTATGATGAACAGCCAAAGTCACAGCTGATT 600
 QY 601 AAGAGGACTGAAGCGGCGGCGGCAAAATACGAATTAA 639
 DB 601 AAGAGGACTGAAGCGGCGGCGGCAAAATACGAATTAA 639
 RESULT 5
 ABK33823
 ID ABK33823 standard; DNA: 639 BP.
 XX
 AC ABK33823;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Bacillus lipase polynucleotide #5.
 XX
 KW Lipase; Bacillus; animal feed; flavour modification; fat modification;
 KW human foodstuff; cheese; food emulsifier; leather tanning; gene; ds;
 KW leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
 KW coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
 KW gastrointestinal lipid related condition; antiinflammatory; respiratory;
 KM gastrointestinal.
 XX
 OS Bacillus circulans.
 XX
 PN W0200206457-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 13-JUL-2001; 2001WO-US22160.
 XX
 PR 13-JUL-2000; 2000US-217954P.
 PR 21-JUN-2001; 2001US-300378P.
 XX
 PA (MAXY-) MAXYGEN INC.
 XX
 PI Giver LJ, Minshull J, Vogel K;
 XX
 DR WPI; 2002-171805/22.
 DR P-PSDB; AAU83845.
 XX
 PT Nucleic acids encoding lipase enzymes which are useful as supplements
 PT in animal feeds, as agents of flavour modification and for treating
 PT Crohn's disease and coeliac disease -
 XX
 PS Claim 81; Page 118-119; 196pp; English.
 XX
 CC The invention relates to new Bacillus lipase enzymes and the nucleic
 CC acids encoding them. The lipase polypeptides are useful as supplements in
 CC animal feeds, as agents of flavour modification and fat modification in
 CC human foodstuffs (e.g. cheese), as agents in the creation of food
 CC emulsifiers, as agents for tanning/processing of leather and as cleaning

CC agents. They are also useful for treating Crohn's disease, cystic
 CC fibrosis, coeliac disease, indigestion, obesity and other
 CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
 CC conditions can be therapeutically or prophylactically treated via a
 CC method of hydrolysing a lipid comprising expressing in a target cell or
 CC contacting a target cell with an effective amount of DNA or protein of
 CC the invention. Sequences ABK3819-ABK3874 represent *Bacillus lipase*
 CC polynucleotides of the invention.

XX Sequence 639 BP; 201 A; 122 C; 157 G; 159 T; 0 other;

Query Match 98.0%; Score 626.2; DB 24; Length 639;
 Best Local Similarity 98.7%; Pred. No. 4.3e-186;
 Matches 631; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 ATGAATTTGTAAGAAAGATCATTCGACTTGAACATTTTGGTGTGACAGTACA 60
 DB 1 ATGAATTTTATAAAGAAAGATCATTCGACTTGAACATTTTGGTGTGACAGTACA 60
 OY 61 TCGCTGTTTGCATGCAGCCGTCAGCAAAAGCCGCTGAACACATTCAGTTGTATGTT 120
 DB 61 TCGCTGTTTGCATGCAGCCGTCAGCAAAAGCCGCTGAACACATTCAGTTGTATGTT 120
 OY 121 CACGCTATCGAGAGAGCTTCATACAAATTTGGGGAAATTAGAGCTATCTGATCTCAG 180
 DB 121 CACGCTATCGAGAGAGCTTCATACAAATTTGGGGAAATTAGAGCTATCTGATCTCAG 180
 OY 121 CACGCTATCGAGAGAGCTTCATACAAATTTGGGGAAATTAGAGCTATCTGATCTCAG 180
 DB 121 CACGCTATCGAGAGAGCTTCATACAAATTTGGGGAAATTAGAGCTATCTGATCTCAG 180
 OY 181 GCGTGTACAGGGGAGAGCTGTATGCGGTTTGGGACAAACAGGCGCAATTT 240
 DB 181 GCGTGTACAGGGGAGAGCTGTATGCGGTTTGGGACAAACAGGCGCAATTT 240
 OY 241 AACCAATGCGCCGATTTATACAGATTTTGCAAAAGGTTTGTAGCAAAACGGGTGCGAAA 300
 DB 241 AACCAATGCGCCGATTTATACAGATTTTGCAAAAGGTTTGTAGCAAAACGGGTGCGAAA 300
 OY 301 AAAGTGAATTTGTGCTCAGAGTATGGGTGCGGACACACCTTACTACTATAAAAT 360
 DB 301 AAAGTGAATTTGTGCTCAGAGTATGGGTGCGGACACACCTTACTACTATAAAAT 360
 OY 361 CTGACGCGGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
 DB 361 CTGACGCGGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
 OY 421 ACAAGCAAGGCGCTTCGCGGAACAGATCCAAATCAAAAGATTTTATACATCATTTTAC 480
 DB 421 ACAAGCAAGGCGCTTCGCGGAACAGATCCAAATCAAAAGATTTTATACATCATTTTAC 480
 OY 481 AGCAATGCGGATATGATGTCATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 540
 DB 481 AGCAATGCGGATATGATGTCATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 540
 OY 541 CAAATTCATGCGGTCGACATTTGTTTATGATGAACAGCAAGTCAACAGCCGTGAT 600
 DB 541 CAAATTCATGCGGTCGACATTTGTTTATGATGAACAGCAAGTCAACAGCCGTGAT 600
 OY 601 AAAGAGAGCTGAACGCGGGGGCCAAATACGAATTA 639
 DB 601 AAAGAGAGCTGAACGCGGGGGCCCTCAATCAATTA 639

RESULT 6
 ABA96150
 ID ABA96150 standard; DNA: 639 BP.

XX ABA96150;

XX 16-Apr-2002 (first entry)

XX *Bacillus circulans lipase 396 gene*.

XX Lipase 396: spore protein application; immune response; HIV; cancer;
 KW autoimmune disorder; inflammatory; allergic reaction; autoantigen;
 KW gene; ds.

XX *Bacillus circulans*.

XX key Location/Qualifiers

XX CDS 1..639

XX /tag= a

XX /product= "lipase 396"

XX MO200200232-A2.

XX 03-JAN-2002.

XX 26-JUN-2001; 2001MO-US20372.

XX 26-JUN-2000; 2000US-214161P.

XX (MAXY-) MAXYGEN INC. Goldman S, Lathrop SJ, Longchamp PF, Whalen RG;

XX WPI: 2002-147853/19.

XX Composition for modulating immune response, comprises a spore system

XX having a spore and polypeptide, carbohydrate or nucleotide sequence

XX having anti-pathogenic activity

XX Example 6: Page 136; 137pp; English.

CC The sequence represents the *Bacillus circulans lipase 396 gene*, which was
 CC inserted into the ColE sequence in the invention. The invention relates
 CC to novel compositions and methods for utilizing spore systems for
 CC medicinal and industrial protein applications. The peptides,
 CC polypeptides, proteins, and nucleic acids of interest in the invention
 CC may be useful for modulating an immune response. A spore system of the
 CC invention may function as a therapeutic, prophylactic, or immunology
 CC agent or vaccine against a disease or disease-inducing pathogen. A spore
 CC system may be designed to display a HIV antigen, or a disease-associated
 CC antigen such as cancer antigens, antigens associated with autoimmunity
 CC disorders, antigens associated with inflammatory conditions, antigens
 CC associated with allergic reactions, antigens associated with infectious
 CC agents, and autoantigens.

XX Sequence 639 BP; 201 A; 122 C; 157 G; 159 T; 0 other;

Query Match 98.0%; Score 626.2; DB 24; Length 639;
 Best Local Similarity 98.7%; Pred. No. 4.3e-186;
 Matches 631; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 1 ATGAATTTGTAAGAAAGATCATTCGACTTGAACATTTTGGTGTGACAGTACA 60
 DB 1 ATGAATTTTATAAAGAAAGATCATTCGACTTGAACATTTTGGTGTGACAGTACA 60
 OY 61 TCGCTGTTTGCATGCAGCCGTCAGCAAAAGCCGCTGAACACATTCAGTTGTATGTT 120
 DB 61 TCGCTGTTTGCATGCAGCCGTCAGCAAAAGCCGCTGAACACATTCAGTTGTATGTT 120
 OY 121 CACGCTATCGAGAGAGCTTCATACAAATTTGGGGAAATTAGAGCTATCTGATCTCAG 180
 DB 121 CACGCTATCGAGAGAGCTTCATACAAATTTGGGGAAATTAGAGCTATCTGATCTCAG 180
 OY 181 GCGTGTACAGGGGAGAGCTGTATGCGGTTTGGGACAAACAGGCGCAATTT 240
 DB 181 GCGTGTACAGGGGAGAGCTGTATGCGGTTTGGGACAAACAGGCGCAATTT 240
 OY 241 AACCAATGCGCCGATTTATACAGATTTTGCAAAAGGTTTGTAGCAAAACGGGTGCGAAA 300
 DB 241 AACCAATGCGCCGATTTATACAGATTTTGCAAAAGGTTTGTAGCAAAACGGGTGCGAAA 300
 OY 301 AAAGTGAATTTGTGCTCAGAGTATGGGTGCGGACACACCTTACTACTATAAAAT 360
 DB 301 AAAGTGAATTTGTGCTCAGAGTATGGGTGCGGACACACCTTACTACTATAAAAT 360
 OY 361 CTGACGCGGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420

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Db 361 CTGACGCGCGAAATTAATGAAACGCTGTAACGCTGGCGGCGGAACCGTTGACG 420
OY 421 ACAAGCAAGCGCTTCGGGGACAGATCCAAATCAAAAATTTTATACATTCATTAC 480
Db 421 ACAAGCAAGCGCTTCGGGGACAGATCCAAATCAAAAATTTTATACATTCATTAC 480
OY 481 AGCAGTCCGATATGATGTCATGAATTAATCAAAATTTAGACGGTGTAAAAAGCT 540
Db 481 AGCAGTCCGATATGATGTCATGAATTAATCAAAATTTAGACGGTGTAAAAAGCT 540
OY 541 CAAATTCATGGCTTGGGACATTTGTTTATGATGAACAGCCAGTCACAGCTGATT 600
Db 541 CAAATTCATGGCTTGGGACATTTGTTTATGATGAACAGCCAGTCACAGCTGATT 600
OY 601 AAGAAGAGCTGAACGGCGGGGCCAAATFACGAATTA 639
Db 601 AAGAAGAGCTGAACGGCGGGGCCCTCAATFACGAATTA 639

RESULT 7
ABK3824
ID ABK3824 standard; DNA: 639 BP.
XX
AC ABK3824;
XX
DT 08-MAY-2002 (first entry)
XX
DE Bacillus lipase polynucleotide #6.
XX
KM Lipase; Bacillus; animal feed; flavour modification; fat modification;
KM human foodstuff; cheese; food emulsifier; leather tanning; gene; ds;
KM leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
KM coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
KM gastrointestinal lipid related condition; anti-inflammatory; respiratory;
KM gastrointestinal.
XX
OS Bacillus azotofomans.
XX
PN WO200206457-A2.
XX
PD 24-JAN-2002.
XX
PF 13-JUL-2001; 2001MO-US22160.
XX
PR 13-JUL-2000; 2000US-217954P.
XX
PR 21-JUN-2001; 2001US-300378P.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Giver LJ, Minshull J, Vogel K;
XX
XX WPI; 2002-171805/22.
XX
XX P-PSDB; AAU83846.
XX
PT Nucleic acids encoding lipase enzymes which are useful as supplements
PT in animal feeds, as agents of flavour modification and for treating
PT Crohn's disease and coeliac disease -
XX
PS Claim 81; Page 119; 196pp; English.
XX
XX The invention relates to new Bacillus lipase enzymes and the nucleic
XX acids encoding them. The lipase polypeptides are useful as supplements in
XX animal feeds, as agents of flavour modification and fat modification in
XX human foodstuffs (e.g. cheese), as agents in the creation of food
XX emulsifiers, as agents for tanning/processing of leather and as cleaning
XX agents. They are also useful for treating Crohn's disease, cystic
XX fibrosis, coeliac disease, indigestion, obesity and other
XX gastrointestinal mal-absorption problems. Gastrointestinal lipid related
XX conditions can be therapeutically or prophylactically treated via a
XX method of hydrolysing a lipid comprising expressing in a target cell or
XX contacting a target cell with an effective amount of DNA or protein of
XX the invention. Sequences ABK3819-ABK3874 represent Bacillus lipase

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CC polynucleotides of the invention.
XX
SQ Sequence 639 BP; 201 A; 121 C; 159 G; 158 T; 0 other;
OY
Query Match 97.5%; Score 623; DB 24; Length 639;
Best Local Similarity 98.4%; Pred. No. 4,4e-185;
Matches 629; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
OY 1 -ATGAATTTTGAANAAGAGATCATTCACCTTGTAACAATTTGGTGTGACAGTACA 60
Db 1 ATGAATTTTGAANAAGAGATCATTCACCTTGTAACAATTTGGTGTGACAGTACA 60
OY 61 TCAGTGTTCGATGACAGCCGTGCAAAAAGCCGCTGAACACATCCAGTTGATGTT 120
Db 61 TCAGTGTTCGATGACAGCCGTGCAAAAAGCCGCTGAACACATCCAGTTGATGTT 120
OY 121 CACGCTATCGAGAGAGCTTCATACAAATTTGGCGAATTAAGCTATTCGTATCTCAG 180
Db 121 CACGCTATCGAGAGAGCTTCATACAAATTTGGGGAATTAAGAGCTATTCGTATCTCAG 180
OY 181 GCGTGTACAGCGGCAAGCTGATGCGTTGATTTTGGGCAAGACAGGACGAATTAAT 240
Db 181 GCGTGTACAGCGGCGAGCTGTATGCGTTGATTTTGGGCAAGACAGGACGAATTAAT 240
OY 241 AACATGCGCCCGGTATATACAGATTTGTGCAAAAAGTTTACAGCAAGCGGTGCAAA 300
Db 241 AACATGCGCCCGGTATATACAGATTTGTGCAAAAAGTTTACAGCAAGCGGTGCAAA 300
OY 301 AACTGTGATATTCGCTGCTCAGATGAGTGGGCGGCAACACCTTACTCATTAATAAT 360
Db 301 AACTGTGATATTCGCTGCTCAGATGAGTGGGCGGCAACACCTTACTCATTAATAAT 360
OY 361 CTGAGACGGCGGAATTAATTTGAAAACGTCGTAAAGCTTGGCGGCGGAACCGTTGACG 420
Db 361 CTGAGACGGCGGAATTAATTTGAAAACGTCGTAAAGCTTGGCGGCGGAACCGTTGACG 420
OY 421 ACAAGCAAGCGCTTCGGGGACAGATCCAAATCAAAAAGTTTATACATTCATTAC 480
Db 421 ACAAGCAAGCGCTTCGGGGACAGATCCAAATCAAAAAGTTTATACATTCATTAC 480
OY 481 AGCAGTCCGATATGATGTCATGAATTAATCAAAATTTAGACGGTGTAAAAAGCT 540
Db 481 AGCAGTCCGATATGATGTCATGAATTAATCAAAATTTAGACGGTGTAAAAAGCT 540
OY 541 CAAATTCATGGCGTTGGGACATTTGTTTATGATGAACAGCCAGTCACAGCTGATT 600
Db 541 CAAATTCATGGCGTTGGGACATTTGTTTATGATGAACAGCCAGTCACAGCTGATT 600
OY 601 -AAGAAGAGCTGAACGGCGGGGCCAAATFACGAATTA 639
Db 601 AAGAAGAGCTGAACGGCGGGGCCCTAGATFACGAATTA 639

RESULT 8
ABK3821
ID ABK3821 standard; DNA: 639 BP.
XX
AC ABK3821;
XX
DT 08-MAY-2002 (first entry)
XX
DE Bacillus lipase polynucleotide #3.
XX
XX Lipase; Bacillus; animal feed; flavour modification; fat modification;
XX human foodstuff; cheese; food emulsifier; leather tanning; gene; ds;
XX leather processing; cleaning agent; Crohn's disease; cystic fibrosis;
XX coeliac disease; indigestion; obesity; gastrointestinal mal-absorption;
XX gastrointestinal lipid related condition; anti-inflammatory; respiratory;
XX gastrointestinal.
XX
XX Bacillus megaterium.
XX
XX WO200206457-A2.
PN

```


XX 24-JAN-2002.
 PD 13-JUL-2001; 2001WO-US22160.
 XX
 PF 13-JUL-2001; 2000US-217954P.
 XX 13-JUL-2000; 2000US-217954P.
 PR 21-JUN-2001; 2001US-300378P.
 XX
 PA (MAXY-) MAXYGEN INC.
 XX
 PI Giver LJ, Minshall J, Vogel K;
 XX
 DR WPI; 2002-171805/22.
 XX P-PSDB; AAU83843.
 XX
 PT Nucleic acids encoding lipase enzymes which are useful as supplements
 PT in animal feeds, as agents of flavour modification and for treating
 PT Crohn's disease and coeliac disease.
 PS Claim 81; Page 117-118; 196pp; English.
 XX
 CC The invention relates to new Bacillus lipase enzymes and the nucleic
 CC acids encoding them. The lipase polypeptides are useful as supplements in
 CC animal feeds, as agents of flavour modification and fat modification in
 CC human foodstuffs (e.g. cheese), as agents in the creation of food
 CC emulsifiers, as agents for tanning/processing of leather and as cleaning
 CC agents. They are also useful for treating Crohn's disease, cystic
 CC fibrosis, coeliac disease, indigestion, obesity and other
 CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
 CC conditions can be therapeutically or prophylactically treated via a
 CC method of hydrolysing a lipid comprising expressing in a target cell or
 CC contacting a target cell with an effective amount of DNA or protein of
 CC the invention. Sequences ABK33819-ABK33874 represent Bacillus lipase
 CC polynucleotides of the invention.
 XX
 SQ Sequence 639 BP; 200 A; 122 C; 158 G; 159 T; 0 other;
 Query Match 94.9%; Score 606.4; DB 24; Length 639;
 Best Local Similarity 98.8%; Pred. No. 7e-180;
 Matches 632; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

QY 1 ATGAATTTGTAAAAAGAGATCATTCGACTTGTATACAAATTTGGTCTGCTAGTCACA 60
 DB 1 ATGAATTTGTAAAAAGAGATCATTCGACTTGTATACAAATTTGGTCTGCTAGTCACA 60
 QY 61 TCGCTGTTGGATGAGCGCTGACGCAAAAGCCGTGACAAATTCAGTATCTGTATGTT 120
 DB 61 TCGCTGTTGGATGAGCGCTGACGCAAAAGCCGTGACAAATTCAGTATCTGTATGTT 119
 QY 121 CAC-GGTATCGAGAGAGCTTACATACAAATTTGCGGAAATTAAGAGCTATCTGTATCTCA 179
 DB 121 CACTGTGATCGAGAGAGCTTACATACATTTTGGCGAAATTAAGAGCTATCTGTATCTCA 179
 QY 180 GGGCTGTGTCAGGGGCAAGCTGTATCGGTTATTTTGGGACACAGGAGCAATTA 239
 DB 180 GGGCTGTGTCAGGGGCAAGCTGTATCGGTTATTTTGGGACACAGGAGCAATTA 239
 QY 240 TAAACATGGCCGGGATTTACAGATTTGTGCAAAAGCTTTAGACGAAGCGGTCCGAA 299
 DB 240 TAAACATGGCCGGGATTTACAGATTTGTGCAAAAGCTTTAGACGAAGCGGTCCGAA 299
 QY 300 AAAAGTGATTTGTCGCTACAGATTTGGTGGCGGACACACCTTACTACATAAAAA 359
 DB 300 AAAAGTGATTTGTCGCTACAGATTTGGTGGCGGACACACCTTACTACATAAAAA 359
 QY 360 TCTGGACGGCGCAATTAATTTGAAAAAGCTGTACGCTTTGGGCGGCAACCGTTGCAC 419
 DB 360 TCTGGACGGCGCAATTAATTTGAAAAAGCTGTACGCTTTGGGCGGCAACCGTTGCAC 419
 QY 420 GACAAGCAAGGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACATCCATTAA 479
 DB 420 GACAAGCAAGGGCTTCGGGGAACAGATCCAAATCAAAAGATTTTATACATCCATTAA 479

QY 480 CAGAGTCCGATATGATTTGCATGATTAATTAATTAAGACGGGTCTAAAAAGCC 539
 DB 480 CAGAGTCCGATATGATTTGCATGATTAATTAATTAAGACGGGTCTAAAAAGCC 539
 QY 540 TCAAAATTCATGGCGTTGGGACATTTGTTTATGATGAACAGCAAGTCACAGCCTGAT 599
 DB 540 TCAAAATTCATGGCGTTGGGACATTTGTTTATGATGAACAGCAAGTCACAGCCTGAT 599
 QY 600 TAAAGAGAGCTGAAACGGCGGCGCAAAATATAGATTTAA 639
 DB 600 TAAAGAGAGCTGAAACGGCGGCGCAAAATATCAAAATTTAA 639
 RESULT 9
 ID AAN70038 standard; DNA; 1831 BP.
 AC AAN70038;
 XX
 DT 02-FEB-1991 (first entry)
 XX
 DE Fragment of pLIP1 insert encoding lipase activity in E.coli.
 XX
 KW Lipase; triglyceride hydrolysisoleic acid; ds.
 XX
 OS Escherichia coli.
 XX
 FH Key Location/Qualifiers
 FT mat_peptide 203..841
 FT /*tag=a
 FT /label=lipase
 XX
 PN EP243338-A.
 XX
 PD 28-OCT-1987.
 XX
 PF 24-APR-1987; 87EP-0870055.
 XX
 PR 25-APR-1986; 86GB-0010230.
 XX
 PA (LABO) LABOFINA S A.
 XX
 DR Vandamme E, Schanck-Brodruck KH, Colson C, Hanotier JUV;
 WPI; 1987-300957/43.
 XX
 PT Production of lipase catalysing triglyceride(s) hydrolysis - is by
 PT using recombinant DNA procedures to give DNA segment coding for
 PT lipase, cloning vectors and yeast or bacterium transformants.
 XX
 PS Disclosure; Fig 2; 19pp; English.
 XX
 CC The DNA sequence encodes recombinant lipase which has the activity
 CC of the known lipase obid. by culturing Geotrichum candidum and is
 CC suitable for similar industrial uses e.g. oleic acid esterification,
 CC as a flavouring agent and in the processing of unsaturated fatty
 CC acid-contg. oils.
 XX
 SQ Sequence 1831 BP; 586 A; 367 C; 416 G; 462 T; 0 other;
 Query Match 88.5%; Score 565.4; DB 8; Length 1831;
 Best Local Similarity 92.8%; Pred. No. 8.1e-167;
 Matches 593; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 1 ATGAATTTGTAAAAAGAGATCATTCGACTTGTATACAAATTTGGTCTGCTAGTCACA 60
 DB 203 ATGAATTTGTAAAAAGAGATCATTCGACTTGTATACAAATTTGGTCTGCTAGTCACA 262
 QY 61 TCGCTGTTGGATGAGCGCTGACGCAAAAGCCGTGACAAATTCAGTATCTGTATGTT 120
 DB 263 TCGCTGTTGGATGAGCGCTGACGCAAAAGCCGTGACAAATTCAGTATCTGTATGTT 322
 QY 121 CACGATTCGAGAGAGCTTACATACAAATTTTGGGGAATTAAGAGCTATCTGTATCTCAG 180

human foodstuffs (e.g. cheese), as agents in the creation of food emulsifiers, as agents for tanning/processing of leather and as cleaning agents. They are also useful for treating Crohn's disease, cystic fibrosis, collic acid disease, indigestion, obesity and other gastrointestinal mal-absorption problems. Gastrointestinal lipid related conditions can be therapeutically or prophylactically treated via a method of hydrolysing a lipid comprising expressing in a target cell or contacting a target cell with an effective amount of DNA or protein of the invention. Sequences ABR33819-ABR33874 represent *Bacillus* lipase polynucleotides of the invention.

Sequence 544 BP; 170 A; 103 C; 141 G; 130 T; 0 other;

Query Match	81.9%	Score 523.2	DB 24	Length 544
Best Local Similarity	97.6%	Pred. No. 8.2e-154		
Matches 531	Conservative	0	Mismatches 13	Indels 0
				Gaps 0

Accession	Gene	Protein	Length	Score	E-value	Identity	Positives	Gaps	Conserved Domains
QY96	TGAACAAATCCAGTTGTATATGATTCACGGTATCGAGAGAGCTTCATATACAAATTTGCGGG		155			100%	155	0	Lipase; Bacillus; animal feed; flavour modification; fat modification; human foodstuff; cheese; food emulsifier; leather tanning; gene; ds; leather processing; cleaning agent; Crohn's disease; cystic fibrosis; coeliac disease; indigestion; obesity; gastrointestinal mal-absorption; gastrointestinal lipid related condition; antiinflammatory; respiratory;
Db1	TGAACAAATCCAGTTGTATATGATTCACGGTATCGAGAGAGCTTCATATCAATTTGCGGG		60			100%	60	0	
QY156	AATTAGAGCTATCTGCTATCTCAAGGCTGGTCAACGGGCGCAAGCTGATGCGGTTGATTT		215			100%	215	0	
Db61	AATTAGAGCTATCTGCTATCTCAAGGCTGGTCAACGGGCGCAAGCTGATGCGGTTGATTT		120			100%	120	0	
QY216	TTGGGCAACAGACAGGAGCAATTAACAATGCGCGGCTATTATCAAGATTTGTGCAAAA		275			100%	275	0	
Db121	TTGGGCAACAGACAGGAGCAATTAACAATGCGCGGCTATTATCAAGATTTGTGCAAAA		180			100%	180	0	
QY276	GGTTTTAGACGAAAACGGGTGCGAAAAAGTGATATTGTCTCACAGTATGGGTGGCGC		335			100%	335	0	
Db181	GGTTTTAGACGAAAACGGGTGCGAAAAAGTGATATTGTCTCACAGTATGGGTGGCGCGC		240			100%	240	0	
QY336	GAACACACCTTACTACATATATAAAATCTGCAGCGCGGCAATTAATTAAGAAACGTCTAAC		395			100%	395	0	
Db241	GAACACACCTTACTACATATATAAAATCTGCAGCGCGGCAATTAATTAAGAAACGTCTAAC		300			100%	300	0	
QY396	GCTTGGCGGCGCGAACCCGTTGACGACACAGCAAGCGCGCTCCGCGGAACAGATCCAAATCA		455			100%	455	0	
Db301	GCTTGGCGGCGCGAACCCGTTGACGACACAGCAAGCGCGCTCCGCGGAACAGATCCAAATCA		360			100%	360	0	
QY456	AAAGATTTTATACATCATTCATTTACACAGCGCGGATATGATTTGTCATGAATTAATTC		515			100%	515	0	
Db361	AAAGATTTTATACATCATTCATTTACACAGCGCGGATATGATTTGTCATGAATTAATTC		420			100%	420	0	
QY516	AAAATTTAGACGGTGTCTAAAAACGCTCAATTCATGGCGTTGGGCAATTTGTTATTTGAT		575			100%	575	0	
Db421	AAAATTTAGACGGTGTCTAAAAACGCTCAATTCATGGCGTTGGGCAATTTGTTATTTGAT		480			100%	480	0	
QY576	GAACAGCAGTCAACGCGCTGATTAAGAAGAGCTCAACGCGGGGGGCCAAANTACGAA		635			100%	635	0	
Db481	GAACAGCAGTCAACGCGCTGATTAAGAAGAGCTCAACGCGGGGGGCCAAANTACGAA		540			100%	540	0	
QY636	TTAA 639								
Db541	TTGA 544								

gastrointestinal.

OS Synthetic.

PN WO200206457-A2.

PD 24-JAN-2002,
YY

PF 13-JUL-2001; 2001WO-US22160.
YY

PR 13-JUL-2000; 2000US-217954P.
PR 21-JUN-2001; 2001US-300378P

XX
PA (MAYY-) MAYYGEN TNC

XX	Giver	I.T.	Minshull
PT			

XX
DR WPT: 2002-171805/22.

DR P-PSDB; AA083893.
XX

PT Nucleic acids encoded in animal feeds, as

Pt Cronin's disease and coeliac disease -

XX

PS CLAIM 81; Page 13/-138; 1986pp; ENGLISH
XX

CC The invention relates to new *Bacillus* lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, colliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences ABR33819-ABR33874 represent *Bacillus* lipase
CC polynucleotides of the invention.

50 Sequence 544 BP; 172 A; 102 C; 138 G; 132 T; 0 other;

Query Match	81.98;	Score 523.2;	DB 24;	Length 544
Best Local Similarity	97.68;	Pred. No. 8.2e-154;		
Matches 531;	Conservative	0;	Mismatches 13;	Indels 0;

QY	96	TGACACAAATCCATTTGTAATAGTTCAACGGATAGGAGGAGACCTTCATACATATTTGGCGG	150
Db	1	TGAACACATCCATTTGTAATAGTTCAACGGATAGGAGGAGACCTTCATACATATTTGGCGG	60
QY	156	AATTAAGAGCATCTCGTATCTCAGGGCTGGTCACGGGGCAGCGTATGCGGTTGATTT	215
Db	61	AATTAAGAGCATCTCGTATCTCAGGGCTGGTCGGGAGACAGCTGATGCGGTTGATTT	120
QY	216	TTGGGACAAAGCAGGAGGACGATTTTAAACATGGCCCGGTATTTACAGATTTGTGCAAA	275
Db	121	TTGGGACAAAGCAGGAGGACGATTTTAAACAAAGCCCGGTATTTACAGATTTGTGCAAA	180
QY	276	GGTTTATGACAAACGGGTGGAAAAAGTGATATGTGCGCTACAGTATGGGTGGCGC	335
Db	181	GGTTTATGACAAACGGGTGGAAAAAGTGATATGTGCGCTACAGCATGGGTGGCGC	240
QY	336	GAACACACCTTACTACATATAAAAAATCTGAGCGCGGAATTAATTAATTAAGAAACGTCGTAC	395
Db	241	GAACACACCTTACTACATATAAAAAATCTGAGCGCGGAATTAATTAATTAAGAAACGTCGTAC	300
QY	396	GCTTTGGCGGCGCGAACCCTTGACGACAGCAGAGGCGCTTCGGGAACAGATCCAAATCA	455
Db	301	ACTTTGGCGGCGCGAATGCTTCGACGACAGCAGAGGCGCTTCGGGAACAGATCCAAATCA	360
QY	456	AAAGATTTTATACACATCCATTTACACAGCGCGGATATGTTCTCAGAAETACTATC	515
Db	361	AAAGATTTTATACACATCCATTTACACAGCGCGGATATGTTCTCAGAAETACTATC	420

[illegible]

Job time : 160 secs

PI Giver LJ, Minshull J, Vogel K;
XX
XX WPI; 2002-171805/22.
DR P-PSDB; AA083883.
XX

PT Nucleic acids encoding lipase enzymes which are useful as supplements
PT in animal feeds, as agents of flavour modification and for treating
PT Crohn's disease and coeliac disease -
XX
XX

PS Claim 81, Page 134, 196pp: English.

XX
XX The invention relates to new Bacillus lipase enzymes and the nucleic
CC acids encoding them. The lipase polypeptides are useful as supplements in
CC animal feeds, as agents of flavour modification and fat modification in
CC human foodstuffs (e.g. cheese), as agents in the creation of food
CC emulsifiers, as agents for tanning/processing of leather and as cleaning
CC agents. They are also useful for treating Crohn's disease, cystic
CC fibrosis, coeliac disease, indigestion, obesity and other
CC gastrointestinal mal-absorption problems. Gastrointestinal lipid related
CC conditions can be therapeutically or prophylactically treated via a
CC method of hydrolysing a lipid comprising expressing in a target cell or
CC contacting a target cell with an effective amount of DNA or protein of
CC the invention. Sequences ABK3819-ABK3874 represent Bacillus lipase
CC polynucleotides of the invention.
XX

SQ Sequence 544 BP: 170 A; 104 C; 140 G; 130 T; 0 other;

Query Match 81.6%; Score 521.6; DB 24; Length 544;
Best Local Similarity 97.4%; Pred. No. 2.6e-153;

Matches 530; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 96 TGAACACATCCAGTCTTATGCTTCACGGTATCGAAGAGCTTCATACATTTTGGCGG 155
DB 1 TGAACACATCCAGTCTTATGCTTCACGGTATCGAAGAGCTTCATACATTTTGGCGG 60
QY 156 AATTAAGAGCTATCTGATCTCAGGGCTGGTCAAGGGCAAGCTGATGGGTTGATT 215
DB 61 AATTAAGAGCTATCTGATCTCAGGGCTGGTCAAGGGCAAGCTGATGGGTTGATT 120
QY 216 TTGGGACACAGACGAGGAGATTTAACAATGCCGCTATTATCAGATTTGCAAAA 275
DB 121 TTGGGACACAGACGAGGAGATTTAACAATGCCGCTATTATCAGATTTGCAAAA 180
QY 276 GCTTTAGAGCAAAAGGGTGGAAAAAGTGATATTGCTCTCAGATATGGGTGGCGC 335
DB 181 GCTTTAGAGCAAAAGGGTGGAAAAAGTGATATTGCTCTCAGATATGGGTGGCGC 240
QY 336 GAACACACCTTACTACATTAATAAATCTGACGCGGAAATTAATTAATAAATGCTGTAAC 395
DB 241 GAACACACCTTACTACATTAATAAATCTGACGCGGAAATTAATAAATGCTGTAAC 300
QY 396 GCTTTGGGCGCGCAAGCGTTCGACGACAGCAAGCGCTTCGGGAAACAGATCCAAATCA 455
DB 301 GCTTTGGGCGCGCAAGCGTTCGACGACAGCAAGCGCTTCGGGAAACAGATCCAAATCA 360
QY 456 AAGGATTTTATACATCCATTTACACAGTCCGATATGATTCATCATTTACTATATC 515
DB 361 AAGGATTTTATACATCCATTTACACAGTCCGATATGATTCATCATTTACTATATC 420
QY 516 AATTAAGAGCTATCTGATCTCAGGGCTGGTCAAGGGCAAGCTGATGGGTTGATT 575
DB 421 AATTAAGAGCTATCTGATCTCAGGGCTGGTCAAGGGCAAGCTGATGGGTTGATT 480
QY 576 GAACAGCAAGCTCAACAGCTGATTTAAGAAGAGACTGAACGGCGGGGCCAAAATACGAA 635
DB 481 GAACAGCAAGCTCAACAGCTGATTTAAGAAGAGACTGAACGGCGGGGCCAAAATACGAA 540
QY 636 TTAA 639
DB 541 TTGA 544

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2003, 06:05:53 ; Search time 43 Seconds
(Without alignments)
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Perfect score: 639
Sequence: 1 atgaatttgtaaaagaag.....ggggcccaataacgaattaa 639

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	297.6	46.6	793	1 US-07-930-678-1	Sequence 1, Appli
2	42.2	6.6	7218	1 US-08-232-463-14	Sequence 14, Appli
3	36.2	5.7	502	4 US-09-280-116-70	Sequence 70, Appli
4	33.2	5.2	1089	3 US-08-978-589A-1	Sequence 1, Appli
5	33.2	5.2	1089	4 US-09-336-601-2	Sequence 2, Appli
6	32.2	5.0	1194	4 US-09-466-257A-7	Sequence 7, Appli
7	32.2	5.0	1194	4 US-09-466-257A-9	Sequence 9, Appli
8	32.2	5.0	1424	1 US-08-723-886-2	Sequence 2, Appli
9	32.2	5.0	1424	4 US-08-424-797A-2	Sequence 9, Appli
10	31.8	5.0	954	4 US-09-134-001C-529	Sequence 529, App
11	31.8	4.9	99500	4 US-09-798-096-10	Sequence 10, Appli
12	30.8	4.8	1684	4 US-08-961-527-258	Sequence 258, App
13	30.8	4.8	6030	1 US-08-441-139-8	Sequence 8, Appli
14	30.4	4.8	289	4 US-09-007-005-17	Sequence 17, Appli
15	30.4	4.8	289	4 US-09-244-796-17	Sequence 17, Appli
16	30.4	4.7	545	4 US-09-227-357-149	Sequence 149, App
17	30	4.7	1194	4 US-09-134-001C-2256	Sequence 2256, Ap
18	29.8	4.7	307	4 US-09-198-083-4	Sequence 4, Appli
19	29.8	4.7	307	4 US-09-862-167-4	Sequence 4, Appli
20	29.8	4.7	3918	3 US-08-836-329-1	Sequence 1, Appli
21	29.8	4.7	5757	4 US-08-984-618-1	Sequence 1, Appli
22	29.6	4.6	6765	2 US-08-677-010-2	Sequence 2, Appli
23	29.6	4.6	6765	2 US-08-790-519-2	Sequence 2, Appli
24	29.6	4.6	9581	2 US-08-677-010-1	Sequence 1, Appli
25	29.6	4.6	9581	2 US-08-790-519-1	Sequence 1, Appli
26	29.4	4.6	816	3 US-08-968-363-8	Sequence 8, Appli
27	29.4	4.6	816	3 US-08-969-683A-8	Sequence 8, Appli

28	29.4	4.6	816	4 US-09-297-928-4	Sequence 4, Appli
29	29.2	4.6	1330	2 US-09-036-582-33	Sequence 33, Appli
30	29.2	4.6	2118	1 US-08-400-422-5	Sequence 5, Appli
31	29.2	4.6	3872	2 US-08-331-081B-4	Sequence 4, Appli
32	29	4.5	1099	4 US-09-072-596-320	Sequence 320, App
33	29	4.5	1716	3 US-08-656-034-9	Sequence 9, Appli
34	29	4.5	2160	3 US-08-656-034-1	Sequence 1, Appli
35	28.6	4.5	711	4 US-09-134-001C-1248	Sequence 1248, Ap
36	28.6	4.5	1524	1 US-08-409-132-1	Sequence 1, Appli
37	28.6	4.5	1524	2 US-08-408-669-1	Sequence 1, Appli
38	28.6	4.5	1720	4 US-08-235-836C-111	Sequence 111, App
39	28.6	4.5	2102	4 US-08-235-836C-65	Sequence 65, Appli
40	28.6	4.5	2107	4 US-08-235-836C-73	Sequence 73, Appli
41	28.6	4.5	2258	1 US-07-720-589-1	Sequence 1, Appli
42	28.6	4.5	2258	2 US-08-785-190-1	Sequence 1, Appli
43	28.6	4.5	2258	5 PCT-US92-05539-1	Sequence 1, Appli
44	28.4	4.4	2900	1 US-08-034-650-9	Sequence 9, Appli
45	28.4	4.4	2900	1 US-08-449-015-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-07-930-678-1
Sequence 1, Application US/07930678
Patent No. 5427936
GENERAL INFORMATION:
APPLICANT: MOELLER, Bernhard
APPLICANT: VETTER, Roman
APPLICANT: WILKE, Detlef
APPLICANT: FOULOIS, Birgit
TITLE OF INVENTION: Alkaline Bacillus Lipases, Coding DNA
TITLE OF INVENTION: Sequences Therefor and Bacilli, Which Produce These
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/930, 678
FILING DATE: 19921013
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP91/00664
FILING DATE: 08-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 40 12 070.8
FILING DATE: 14-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, J.D.
REGISTRATION NUMBER: 26, 269
REFERENCE/DOCKET NUMBER: 16877/318/KACH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)836-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:
ORGANISM: Bacillus pumilus DSM 5776
STRAIN: DSM 5776
FEATURE:
NAME/KEY: sig-peptide
LOCATION: 126..221
FEATURE:
NAME/KEY: mat-peptide
LOCATION: 222..764
FEATURE:
NAME/KEY: cds
LOCATION: 126..764
US-07-930-678-1

Query Match 46.6%; Score 297.6; DB 1; Length 793;
Best Local Similarity 66.9%; Pred. No. 7.8e-89;
Matches 423; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

QY 8 TTGTAAAAAGAGATCATTCGACTTTGACAAATTTGGTGTCTGCTCAGTCACATCGCTGT 67
DB 136 TTAAAGAAAGAGATTGCCAAATTCCTACATTCGCTTGCATTTGGTATGTTCAATGGCGT 195
QY 68 TTGGATGACGCGCTGCAAAAGCCGTGACACATTCAGTTGTTATGGTTACGGTA 127
DB 196 TTATCCAGCCGAAAGAGCGGAGCGGCTGACATATCCGGTTGTATGTCAGCGCA 255
QY 128 TCGAGAGAGCTTCATACAAATTTGGGGAATTAAGACATCTCTGATCTCAGGCGTGT 187
DB 256 TTGGCGGTGCTCTTATTAACGTTTTTTCTATTAAGTTATTTGGCACACAAAGCGTGG 315
QY 188 CAGGGGCAAGCTGTATGCGGTGATTTTGGACAGACAGGACCAATTTATACATG 247
DB 316 ATCGAAACATTAATATGATTTGATTTTCAAGCAAAAGCAAAATTAACCGCAATG 375
QY 248 GCCCGTATTTATACGATTTTGTCAAAAGTTTGAAGCAAAAGCGTGCAGAAAGTGG 307
DB 376 GTCCGCTCATGAGATTTGTCAAAAGTGTGAAGCAAAAGCGGCGCAAAAGTAG 435
QY 308 ATATTTGCTCAGATATGAGTGGTGGCGGCAACACCTTACTACATATAAATTTGGACG 367
DB 436 ATATTTGCTCAGATATGAGTGGTGGCGGCAACACCTTACTACATATAAATTTAGATG 495
QY 368 GCGGAAATTAATTAAGAGCTGTAGCGTTGGCGGCGGAAACCGTTGACGACAGCA 427
DB 496 GCGGCGATTAATTAAGAGCTGTAGCGTTGGCGGCGGAAACCGTTGACGACAGCA 555
QY 428 AGCGGCTTCGCGGAAAGATCAAAAGATTTTATACATTCATTTACAGCAGTG 487
DB 556 GAGCATTAACAGGACGATCAAAATCAAAATTTTACATTCGCTATAGCTCAG 615
QY 488 CCGATATGATTTGATGATTAATTTATCAAAATTAAGCGGTGCTAAAGCGCTCAATTC 547
DB 616 CAATATCTAATTTGCTCAAGCGCTCTGTTAATTTGGCGCAAGAAATCTGTATCC 675
QY 548 ATGGCGTTGGGACATGTTTATTTATGAAGCGCAAGTCAACAGCGCTGTTAAAGAG 607
DB 676 ATGGCGTTGGTCAATGCTGTTAATTAACCTCAAGCGCAAGTGAAGGATATTTAAAGAG 735
QY 608 GACTGAAGCGGCGGCGCAAAATTAAGATTA 639
DB 736 GACTGAAGCGGCGGCGCAAAATTAAGATTA 767

RESULT 2
US-08-232-463-14/C
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
City: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEO ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ9pt-F15
US-08-232-463-14

Query Match 6.6%; Score 42.2; DB 1; Length 7218;
Best Local Similarity 1.3%; Pred. No. 0.001;
Matches 5; Conservative 214; Mismatches 152; Indels 0; Gaps 0;

QY 265 TTGTGCAAAAGGTTTGAAGCAAGCGGTGCGCAAAAGTGTATTCGCTCAGT 324
DB 1441 TTGGTACRR 1382
QY 325 ATGGGTGCGCGAAGACACCTTACTACATAAAATCTGACGCGGAAATTAATGAA 384
DB 1381 RRR 1222
QY 385 AACGTGTAACGCTTGGCGGCGAAGCGTTGACGACGAAGCAAGCGCTTCGGGACA 444
DB 1321 RRR 1262
QY 445 GATCCCAATCAAAAGATTATACATCATTCATTTAGCAGTGGCGGATATGATTCATG 504
DB 1261 RRR 1202
QY 505 AATTACTTATCAAAATTAAGAGCGTGAATAAACGCTCAATTCATGCTTGGACAT 564
DB 1201 RRR 1142
QY 565 GGTATATGATGAACAGCAAGCTCAACAGCGCTGATTAAGAGAGTGAAGCGGCGG 624
DB 1141 RRR 1082
QY 625 CAAATACGAA 635
DB 1081 RRRRRRRRRRR 1071

RESULT 3

RESULT 4
 US-08-978-589A-1
 Sequence 1, Application US/08978589A
 Patent No. 6087145
 GENERAL INFORMATION:
 APPLICANT: ISHII, Takeshi
 APPLICANT: MITSUO, Satoshi
 TITLE OF INVENTION: ESTERASE GENE AND ITS USE
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
 STREET: P.O. BOX 747
 CITY: FALLS CHURCH
 STATE: VIRGINIA
 COUNTRY: UNITED STATES OF AMERICA
 ZIP: 22040
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/978,589A
 FILING DATE: 26-NOV-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Murphy Jr, Gerald M.
 REGISTRATION NUMBER: 28,977
 REFERENCE/DOCKET NUMBER: 20-4336P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 205-8000
 TELEFAX: (703) 205-8050
 INFORMATION FOR SEQ ID NO: 1:

US-09-466-257A-7
 RESULT 6
 * Sequence 7, Application US/09466257A-7
 * Patent No. 6337190
 * GENERAL INFORMATION:
 * APPLICANT: Hwang, Tzann-Shun
 * APPLICANT: Wu, Szu-Pei
 * APPLICANT: Chou, Hsin-Hua
 * APPLICANT: Hwa-Yi
 * APPLICANT: Lin, Lung-Shen

APPLICANT: Tsai, Hsin
APPLICANT: Chang, Edward
TITLE OF INVENTION: A No. 6337190e1 D-Amino Acid Amino transferase For
TITLE OF INVENTION: Simultaneously Producing
TITLE OF INVENTION: Glutaryl-7-Aminocephalosporanic Acid And D-Amino Acid
FILE REFERENCE: 1476-4003
CURRENT APPLICATION NUMBER: US/09/466,257A
CURRENT FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 7
LENGTH: 1194
TYPE: DNA
ORGANISM: Bacillus sphaericus
US-09-466-257A-7

Query Match
Best Local Similarity 53.6%; Pred. No. 0.8; Length 1194;
Matches 67; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 425 GCAAGGCGCTTCGCGGAACAGATCCAAATCAAAAGATTATTAACATCCATTACAGCA 484
DB 588 GCGGCGTACTTCGGAACAAGACATCTGAAAAGTTGTACGAAGCCATTACACC 647
QY 485 GTGCCGATATGATGTCATGATTAATTAATTAAGACGCTGCTAAACGCTCAA 544
DB 648 GTGGAGATATTAATCAAGAAATGTTCTGCTAATGCTATGATTAAGATGTAAC 707
QY 545 TTTCAT 549
DB 708 TTTAT 712

RESULT 7
US-09-466-257A-9
Sequence 9, Application US/09466257A
Patent No. 6337190
GENERAL INFORMATION:
APPLICANT: Hwang, Tzann-Shun
APPLICANT: Wu, Szu-Pei
APPLICANT: Chou, Hsin-Hua
APPLICANT: Chen, Hwa-Yi
APPLICANT: Lin, Lung-Shen
APPLICANT: Tsai, Hsin
APPLICANT: Chang, Edward
TITLE OF INVENTION: A No. 6337190e1 D-Amino Acid Amino transferase For
TITLE OF INVENTION: Simultaneously Producing
TITLE OF INVENTION: Glutaryl-7-Aminocephalosporanic Acid And D-Amino Acid
FILE REFERENCE: 1476-4003
CURRENT APPLICATION NUMBER: US/09/466,257A
CURRENT FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 9
LENGTH: 1194
TYPE: DNA
ORGANISM: Bacillus sphaericus
US-09-466-257A-9

Query Match
Best Local Similarity 53.6%; Pred. No. 0.8; Length 1194;
Matches 67; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 425 GCAAGGCGCTTCGCGGAACAGATCCAAATCAAAAGATTATTAACATCCATTACAGCA 484
DB 588 GCGGCGTACTTCGGAACAAGACATCTGAAAAGTTGTACGAAGCCATTACACC 647
QY 485 GTGCCGATATGATGTCATGATTAATTAATTAAGACGCTGCTAAACGCTCAA 544
DB 648 GTGGAGATATTAATCAAGAAATGTTCTGCTAATGCTATGATTAAGATGTAAC 707
QY 545 TTTCAT 549
DB 708 TTTAT 712

DB 708 TTTAT 712

RESULT 8

US-08-723-896-2
Sequence 2, Application US/08723896
Patent No. 572855
GENERAL INFORMATION:
APPLICANT: Fotheringham, Ian G.
APPLICANT: Taylor, Paul P.
APPLICANT: Ton, Jennifer L.
TITLE OF INVENTION: Preparation of D-Amino acids by Direct
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitzpatrick, Cella, Harper & Scinto
STREET: 277 Park Avenue
CITY: New York
STATE: NY
COUNTRY: United States of America
ZIP: 10172-0194
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,896
FILING DATE:
CLASSIFICATION: 435
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-2400
TELEFAX: 212-758-2982
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1424 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 427..1275
US-08-723-896-2

Query Match
Best Local Similarity 53.6%; Pred. No. 0.87; Length 1424;
Matches 67; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 425 GCAAGGCGCTTCGCGGAACAGATCCAAATCAAAAGATTATTAACATCCATTACAGCA 484
DB 881 GCGGCGTACTTCGGAACAAGACATCTGAAAAGTTGTACGAAGCCATTACACC 940
QY 485 GTGCCGATATGATGTCATGATTAATTAATTAAGACGCTGCTAAACGCTCAA 544
DB 941 GTGGAGATATTAATCAAGAAATGTTCTGCTAATGCTATGATTAAGATGTAAC 1000
QY 545 TTTCAT 549
DB 1001 TTTAT 1005

RESULT 9

US-08-424-797A-2
Sequence 2, Application US/08424797A
Patent No. 6358714
GENERAL INFORMATION:
APPLICANT: Fotheringham, Ian G.
APPLICANT: Taylor, Paul P.
APPLICANT: Yoshida, Roberta K.
TITLE OF INVENTION: Materials and Methods for the
NUMBER OF SEQUENCES: 19

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;; STREET: 233 South Wacker Drive, 6300 Sears Tower
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: United States of America
;; ZIP: 60606-6402
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: Patent Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/424,797A
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meyers, Thomas C.
;; REGISTRATION NUMBER: 36,989
;; REFERENCE/DOCKET NUMBER: 27127/32582
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312-474-6300
;; TELEFAX: 312-474-0448
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1424 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 427..1278
;; US-08-424-797A-2

Query Match
Best Local Similarity 5.0%; Score 32.2; DB 4; Length 1424;
Matches 67; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 425 GCAAGCGCTTCGGGACACATCAATCAAAAGATTTTATACATCCATTACAGCA 484
DB 881 GCGCGGTACTTGGCAAGACAGACATCTGAAGAGGTTGTCGAGGCCATTTCACCC 940
QY 485 GTCCGATATGATGTTCATGATTAATCAAAATTTAGACGGTGTAAAGCGTCAAA 544
DB 941 GTGAGATATTTATCAGAGATGTTCTTCGCTAATGCTATGATTAAGATGTAAC 1000
QY 545 TGCAT 549
DB 1001 TTTAT 1005

RESULT 10
US-09-134-001C-529/c
; Sequence 529, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 529
; LENGTH: 954
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; US-09-134-001C-529

Query Match
Best Local Similarity 5.0%; Score 31.8; DB 4; Length 954;
Matches 51; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 455 AAAAGATTTTATACATCATTTTACAGCAGTCCGATATGATGTCATGATTAAT 514
DB 920 ACAAGATTGTCAAAATATTTTACAGGTGTAGCATATGATTCCTTCCCTAATTTA 861
QY 515 CAAATTTAGACGGTGTCAAAAC 537
DB 860 CTAAGTCCTCATTAATATATC 838

RESULT 11
US-09-798-096-10
; Sequence 10, Application US/0798096
; Patent No. 6399378
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; TITLE OF INVENTION: ANTISENSE MODULATION OF REGQ2 EXPRESSION
; FILE REFERENCE: RTS-0207
; CURRENT APPLICATION NUMBER: US/09/798,096
; CURRENT FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 10
; LENGTH: 99500
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; US-09-798-096-10

Query Match
Best Local Similarity 4.9%; Score 31; DB 4; Length 99500;
Matches 103; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 226 ACAGGACGATTTTAAACATGCGCGGTATTCACGATTTGCAAAAGTTTAGAC 285
DB 21734 ACAAGGGACATTTATACATGATTTACAGAGTAAAGATTTATAGAGATTTGAG 21793
QY 286 GAAAGGGGTGCGAAAAAGTGATATGTCCTACAGATVGGGTGGCGGAACACCT 345
DB 21794 CAATGATGCCAACAAATTTGATTAACATGAATGAATGATTAATCTCCCAACACAT 21853
QY 346 TACTACATTAATAATCTGACGGCGGAAATTAATTAACCTGTACAGCTTGGCGGC 405
DB 21854 AACCCACCAAGACAGAAATCATGAAGAAACAGAAATCTGAACAGACCTATAGTAAGG 21913
QY 406 GCGAACGTTTCAGACAGCAAGCGCTCCGGAACAGATC 448
DB 21914 AGATTGAGTTAGTATCAGGTATCACCACCAAGAAAGAAAGCTC 21956

RESULT 12
US-08-961-527-258
; Sequence 258, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; OPERATING SYSTEM: HP Vectra 486/33
; MSDOS version 6.2

QY	Db	QY	Db
384	AAAGCTGCTAACGCTTGGCGCGCGAACCCTTCACACACAAGCGCTTCCGGGAAAC	443	
147	RNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRS	206	
444	AGATCCAAA	452	
207	RNRNRSRNR	215	

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RESULT 15
US-09-244-796-17
: Sequence 17, Application US/09244796
: Patent No. 6281344
:
GENERAL INFORMATION:
: APPLICANT: Szostak, Jack W.
: APPLICANT: Roberts, Richard W.
: APPLICANT: Liu, Rihе
:
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350007
:
CURRENT APPLICATION NUMBER: US/09/244,796
CURRENT FILING DATE: 1999-02-05
:
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
:
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
:
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER FILING DATE: 1998-01-14
:
NUMBER OF SEQ. ID NOS: 33
:
SOFTWARE: fastSeq for Windows Version 4.0
:
SEQ. ID NO 17
:
LENGTH: 289
:
TYPE: RNA
:
ORGANISM: Artificial Sequence
:
FEATURE:
:
OTHER INFORMATION: Translation template
:
FEATURE:
:
NAME/KEY: misc_feature
:
LOCATION: (1)...(289)
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OTHER INFORMATION: n = A,T,C or G
:
US-09-244-796-17

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[illegible]

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GenCore version 5.1.4.p5.4578
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Gapop 10.0 , Gapext 1.0

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published_Applications_NA:*
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14: /cgn2-6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	38.2	6.0	1011	9 US-09-878-781-9	Sequence 11, Appl1
3	38.2	6.0	1011	10 US-09-878-766a-17	Sequence 19, Appl1
4	37.4	5.9	400	7 US-08-781-986a-4008	Sequence 4008, Ap
5	37.4	5.9	13321	7 US-08-781-986a-4	Sequence 4, Appl1
6	35.8	5.6	785	9 US-09-991-936-852	Sequence 852, App
7	34.6	5.4	749	9 US-09-938-842a-3605	Sequence 3605, Ap
8	34.4	5.4	32768	10 US-09-070-927a-128	Sequence 128, App
9	33.8	5.3	546	9 US-10-184-644-412	Sequence 412, App
10	33.8	5.3	546	9 US-10-184-634-412	Sequence 412, App
11	33.2	5.2	597	10 US-09-917-800a-846	Sequence 412, App
12	33.2	5.2	1089	9 US-10-147-467-1	Sequence 412, App
13	32.8	5.1	536165	9 US-09-939-964-1	Sequence 1, Appl1
14	32.6	5.1	1884	10 US-09-731-872-18	Sequence 1, Appl1
15	32.2	5.0	432	10 US-09-974-300-1896	Sequence 1896, Ap
16	31.2	4.9	382	10 US-09-880-107-667	Sequence 667, App
17	31.2	4.9	1180	10 US-09-881-752a-195	Sequence 195, App
18	31	4.9	694	9 US-10-184-644-60	Sequence 60, Appl1
19	31	4.9	694	9 US-10-184-634-60	Sequence 60, Appl1

20	30.8	4.8	737	10 US-09-770-149-76	Sequence 76, Appl1
21	30.8	4.8	1011	9 US-09-878-781-11	Sequence 11, Appl1
22	30.8	4.8	1011	10 US-09-878-766a-19	Sequence 19, Appl1
23	30.8	4.8	2000	9 US-09-938-842a-3864	Sequence 3864, Ap
24	30.6	4.8	402	9 US-09-918-995-36871	Sequence 36871, A
25	30.6	4.8	1101	10 US-09-770-445-100	Sequence 100, App
26	30.6	4.8	1404	10 US-09-912-020-221	Sequence 221, App
27	30.6	4.8	1939	9 US-09-954-531-382	Sequence 382, App
28	30.2	4.7	433	10 US-09-867-926-1711	Sequence 1711, Ap
29	30.2	4.7	500	9 US-09-991-936-1676	Sequence 1676, Ap
30	30.2	4.7	594	9 US-10-123-155-10	Sequence 10, Appl1
31	30.2	4.7	2673	9 US-10-092-154-1876	Sequence 1876, Ap
32	30.2	4.7	2673	10 US-09-764-847-1876	Sequence 1876, Ap
33	30.2	4.7	249487	9 US-10-026-188-3	Sequence 3, Appl1
34	30.2	4.7	545	9 US-09-983-802-149	Sequence 149, App
35	30	4.7	83450	9 US-09-811-469-3	Sequence 3, Appl1
36	29.8	4.7	307	9 US-10-105-877-4	Sequence 4, Appl1
37	29.8	4.7	320	10 US-09-783-590-8898	Sequence 8898, Ap
38	29.8	4.7	400	7 US-08-781-986a-3578	Sequence 3578, Ap
39	29.8	4.7	545	10 US-09-864-761-8107	Sequence 8107, Ap
40	29.8	4.7	12658	7 US-08-781-986a-127	Sequence 127, App
41	29.6	4.6	1184	9 US-10-123-155-412	Sequence 412, App
42	29.6	4.6	5598	9 US-09-938-842a-1436	Sequence 1436, App
43	29.6	4.6	15856	9 US-09-764-891-8240	Sequence 8240, Ap
44	29.6	4.6	1691139	9 US-10-067-514-1	Sequence 1, Appl1
45	29.4	4.6	549	9 US-09-991-936-476	Sequence 476, App

ALIGNMENTS

RESULT 1
US-10-028-247-3
Sequence 3, Appl1 Application US/10028247
Patient No. US20020150594A1
GENERAL INFORMATION:
APPLICANT: Goldman, Stanley
APPLICANT: Lathrop, Stephanie J.
APPLICANT: Longchamp, Pascal F.
APPLICANT: Whalen, Robert G.
TITLE OF INVENTION: Methods and Compositions for Developing Score Display
TITLE OF INVENTION: Systems for Medicinal and Industrial Applications
FILE REFERENCE: 18097a-03352005
CURRENT APPLICATION NUMBER: US/10-028,247
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US-60/214,164
PRIOR FILING DATE: 2000-06-26
PRIOR APPLICATION NUMBER: US 09/892,208
PRIOR FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 639
TYPE: DNA
ORGANISM: Bacillus circulans
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(639)
OTHER INFORMATION: Lipase 396
US-10-028-247-3

Query Match 98.0% Score 626.2; DB 12; Length 639;
Best Local Similarity 98.7%; Pred No. 9.3e-187;
Matches 631; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 ATGAATTTGTAAGAAAGATCATTCGACTTGTACAAATTTGCTGCTACACACA 60
|||||
DB 1 ATGAATTTATTAAGAAAGATCATTCGACTTGTACAAATTTGCTGCTACACACA 60
|||||
QY 61 TCGCTGTTTGGATGACGCGGTACGAAAGCGCGTGAACACAAATTCAGTTTATGCTT 120
|||||
DB 61 TCGCTGTTTGGATGACGCGGTACGAAAGCGCGTGAACACAAATTCAGTTTATGCTT 120
|||||

QY 121 CACGATATCGAGAGAGCTTCATACATTTTCGGGAATTAAGACCTATCTGTAATCTCAG 180
|||
Db 121 CACGATATCGAGAGAGCTTCATACATTTTCGGGAATTAAGACCTATCTGTAATCTCAG 180
QY 181 GCGTGTGACGCGGCGCAAGCTATATCGGTTATTTTGGCAAGACAGGAGCAATAT 240
|||
Db 181 GCGTGTGACGCGGCGCAAGCTATATCGGTTATTTTGGCAAGACAGGAGCAATAT 240
QY 241 AACATATGCGCGGATTTATATCAGATTTGTGCAAAAAGTTTATAGCAAGAGGTCGCAAA 300
|||
Db 241 AACATATGCGCGGATTTATATCAGATTTGTGCAAAAAGTTTATAGCAAGAGGTCGCAAA 300
QY 301 AAATGATATTTGCTCTACAGATATGGTGGCGGCAACACCTTACTACATAAAAAAT 360
|||
Db 301 AAATGATATTTGCTCTACAGATATGGTGGCGGCAACACCTTACTACATAAAAAAT 360
QY 361 CTGACGCGGCAATTAATTAAGATGCTAAGCGTGGCGGCGGCAACCGTTCGACG 420
|||
Db 361 CTGACGCGGCAATTAATTAAGATGCTAAGCGTGGCGGCGGCAACCGTTCGACG 420
QY 421 ACAAGCAAGCGCTTCCGGCAACAGATCCAAATCAAAAGATTTTATACATCCATTAC 480
|||
Db 421 ACAAGCAAGCGCTTCCGGCAACAGATCCAAATCAAAAGATTTTATACATCCATTAC 480
QY 481 AGCAGTCCGATATGATTTGCTATCAATTTACTATCAAAATAGACGGTCTAAAAACGCT 540
|||
Db 481 AGCAGTCCGATATGATTTGCTATCAATTTACTATCAAAATAGACGGTCTAAAAACGCT 540
QY 541 CAATATGATGCGCTTGGGACATGCTTTATTTGATGAACAGCCCAAGCCTGATT 600
|||
Db 541 CAATATGATGCGCTTGGGACATGCTTTATTTGATGAACAGCCCAAGCCTGATT 600
QY 601 AAAGAGAGCTGAAGCGGCGGCAAAATAGCAATTA 639
|||
Db 601 AAAGAGAGCTGAAGCGGCGGCAAAATAGCAATTA 639
RESULT 2
US-09-878-781-9
Sequence 9, Application US/09878781
Publication No. US20030082781A1
GENERAL INFORMATION:
APPLICANT: Bolton, Alexandra J.
APPLICANT: Perez-Casal, Jose
APPLICANT: Fontaine, Michael
APPLICANT: Potter, Andrew A.
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH GAPC PROTEIN AGAINST
FILE REFERENCE: 9000-0055
CURRENT APPLICATION NUMBER: US/09/878,781
CURRENT FILING DATE: 2002-09-10
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 1011
TYPE: DNA
ORGANISM: Streptococcus parauberis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1011)
US-09-878-781-9
Query Match 6.08: Score 38.2; DB 9; Length 1011;
Best Local Similarity 56.98; Pred. No. 0.13;
Matches 70; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
QY 267 TGTCCAAAAGGTTTACGCAAGCGGCGCAAAAAGTGTATTTGCGCTACAGAT 326
|||
Db 315 TGTCCAAAACATTACATGAAATGGCTAAAGATTTTATCACTGCTCGTG 374
QY 327 GCGTGGCGGCAACACCTTACTACATTAATAATCTGACGCGGCAATTAATTA 386
|||
Db 327 GCGTGGCGGCAACACCTTACTACATTAATAATCTGACGCGGCAATTAATTA 386

Db 375 AGATGACGTGAACACAGTTGATTTAACTAACCATGATATCTTATGAGAACTGAAC 434
QY 387 CGT 389
|||
Db 435 AGT 437
RESULT 3
US-09-878-766A-17
Sequence 17, Application US/09878766A
Patent No. US20020044928A1
GENERAL INFORMATION:
APPLICANT: Potter, Andrew A.
APPLICANT: Perez-Casal, Jose
APPLICANT: Fontaine, Michael
TITLE OF INVENTION: IMMUNIZATION OF DAIRY CATTLE WITH CHIMERIC GAPC PROTEIN
FILE REFERENCE: 9000-0057
CURRENT APPLICATION NUMBER: US/09/878,766A
CURRENT FILING DATE: 2001-09-10
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 1011
TYPE: DNA
ORGANISM: Streptococcus parauberis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1011)
US-09-878-766A-17
Query Match 6.08: Score 38.2; DB 10; Length 1011;
Best Local Similarity 56.98; Pred. No. 0.13;
Matches 70; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
QY 267 TGTCCAAAAGGTTTACGCAAGCGGCGCAAAAAGTGTATTTGCGCTACAGAT 326
|||
Db 315 TGTCCAAAACATTACATGAAATGGCTAAAGATTTTATCACTGCTCGTG 374
QY 327 GCGTGGCGGCAACACCTTACTACATTAATAATCTGACGCGGCAATTAATTA 386
|||
Db 375 AGATGACGTGAACACAGTTGATTTAACTAACCATGATATCTTATGAGAACTGAAC 434
QY 387 CGT 389
|||
Db 435 AGT 437
RESULT 4
US-08-781-986A-4008
Sequence 4008, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
FILING DATE:
APPLICATION NUMBER: US/08/781,986A
CLASSIFICATION: 435
PRIOR APPLICATION DATA:


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: TOPOLOGY: Linear
US-08-761-986A-4

Query Match          5.9%; Score 37.4; DB 7; Length 13321;
Best Local Similarity 53.8%; Pred. No. 1;
Matches 77; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 447 TCCAAATCAAAAGATTTTATACATCCATTTACAGCAGTGGCGATATGATGTGTCATGAA 506
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 5746 TACAAACCAACAAAAGCTCTTAACATTTGTTTAAACCAATGCTTGAAGCTTTCTAATAT 5805
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 507 TTACTTATCAAAATTTAGACGGTGTCTAAACGCTCAAAATTCATGGCGTTGGGCACATTGG 566
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 5806 TTTATGCTTTTAAAGATTAAGTACTGTGTATCTACAGATGACCTTAACCGTCTTAAATAC 5855
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 567 TTATTGATGAACAGCCAAATGCA 589
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 5866 CTGCGTGATTTGATTAACCAAAATGA 5888

RESULT 6
US-09-991-936-852/c
; Sequence 852, Application US/09991936
; Publication No. US20030073827A1
; GENERAL INFORMATION:
; APPLICANT: Brandt, Kevin S.
; APPLICANT: Gaines, Patrick J.
; APPLICANT: Stinchcomb, Dan T.
; APPLICANT: Wisniewski, Nancy
; TITLE OF INVENTION: FLEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE
; FILE REFERENCE: FC-6-01
; CURRENT APPLICATION NUMBER: US/09/991,936
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US/09/543,668
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/128,704
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1959
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 852
; LENGTH: 549
; TYPE: DNA
; ORGANISM: Ctenocephalides felis
US-09-991-936-852

Query Match          5.6%; Score 35.8; DB 9; Length 549;
Best Local Similarity 49.7%; Pred. No. 0.54;
Matches 91; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 453 TCAAAAGATTTTATACATCCATTTACAGCAGTGGCATATGATTGTGATGAAATTA 512
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 501 TCAAGTTATTTATCTCAGTAAACATCATTTTAAACAATATTATCTTAATGATATGTA 442
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 513 ATCAAAATTTAGCGGTGCTAAACAGCGTCAAATTTATGCGCGTTGGGCACATTGTTT 572
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 441 TGCACACAAATTTTGTCTAAATATGTTTAAATTTTACATGTCGTGATTAATAATTA 382
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 573 GATGAACAGCCAAAGTCACACAGCTCATTTAAAGAAAGACTGAACGGCGGCGCAAAATAC 632
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 381 AATAAATAATGCCAGTAATAATAGTAACCTTAATTAATATTTTATTTGACAATAATCA 322
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 633 GAA 635
      ||
DB 321 CAA 319

RESULT 7
US-09-938-842A-3605/c
; Sequence 3605, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff

```



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Db 305 .DBCHABH..MS.NSM.Y.BM.YM..Y.CH.B.RYNN.TS.NCA.D....AM.SR.W. 246
OY 435 TCCGGGACAGATCCCAATCAAAAGATTATTATACATCATCTTACAGCAGCGCCATAT 494
Db 245 ..M.HA.M.D..TY..T.T..TTADR.W..M.CA..T.S..ABH....M.B 186
OY 495 GATGTGATGATTAATTCATTAATAATTAGACGGTGTAAAGCGCTCAATTCATGCGCT 554
Db 165 ..B.H.BAH..CS.K.D..MH.TNMA.Y.Y.MH.AM.NN.N..Y.MN.SB.S..BT. 126
OY 555 TGGGACATTTGGTTTATGATGACAGCCAGCTCAACGCTGATTAAGAAGACTGAA 614
Db 125 YMSR..HR.H..D.K.T.HNMBH..HSRSS..Y.S..SMM.SY.KW.AKRG..CR.. 66
OY 615 CGCGGGGGCCCAA 628
Db 65 B.S.R.ST..M..A 52
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RESULT 10

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US-10-184-634-412/C
; Sequence 412, Application US/10184634
; Publication No. US2003006864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C217
; CURRENT APPLICATION NUMBER: US/10/184,634
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 412
; LENGTH: 546
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-634-412
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Query Match 5.3%; Score 33.8; DB 9; Length 546;
Best Local Similarity 7.0%; Pred. No. 2.3;
Matches 26; Conservative 96; Mismatches 252; Indels 0; Gaps 0;
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OY 255 ATATACACGATTTGGCAAAAGCTTTTACAGCAACGGGTGGGAAAAAGTGATTTCT 314
Db 425 RY.MGR..A..M..MNYN.R.Y..NA.NC.....RT.DNRM.M.GA.YD.D..S.... 366
OY 315 CCTCACAGTATGGTGGCGGACACACCTTACTACTATAAAATCTGACGGCGGAAA 374
Db 365 .AM.NNHM.H....ND.S..SD..Y..HGY.....A.NTKM.SN.B..MAC.NN.S.M. 306
OY 375 TAAATTTGAAAAGCTGTACAGCTTTGGCGCGGAGAACCGCTGCAGCAAGAGCGCT 434
Db 305 .DBCHABH..MS.NSM.Y.BM.YM..Y.CH.B.RYNN.TS.NCA.D....AM.SR.W. 246
OY 435 TCCGGGACAGATCCCAATCAAAAGATTATTATACATCATCTTACAGCAGCGCCATAT 494
Db 245 ..M.HA.M.D..TY..T.T..TTADR.W..M.CA..T.S..ABH....M.B 186
OY 495 GATGTGATGATTAATTCATTAATAATTAGACGGTGTAAAGCGCTCAATTCATGCGCT 554
Db 165 ..B.H.BAH..CS.K.D..MH.TNMA.Y.Y.MH.AM.NN.N..Y.MN.SB.S..BT. 126
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OY 555 TGGGACATTTGGTTTATGATGACAGCCAGCTCAACGCTGATTAAGAAGACTGAA 614
Db 125 YMSR..HR.H..D.K.T.HNMBH..HSRSS..Y.S..SMM.SY.KW.AKRG..CR.. 66
OY 615 CGCGGGGGCCCAA 628
Db 65 B.S.R.ST..M..A 52
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RESULT 11

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US-09-917-800A-846/C
; Sequence 846, Application US/09917800A
; Patent No. US20020119462A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Castile, Arthur
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 846
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 A1169239
US-09-917-800A-846
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Query Match 5.2%; Score 33.2; DB 10; Length 597;
Best Local Similarity 56.4%; Pred. No. 3.7;
Matches 62; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
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OY 243 CAATGGCCGGTATTATCATCAATTTGTGCAAAAGTTTATAGCAAAAGCGTGCAGAAA 302
Db 396 CATTAAATTTGCATTTACTTCTTGGGAAAAACATTTTGGAGAACGATAGAAAAAC 337
OY 303 AGTGAATATTGTCGCTACAGATGATGGTGGCGGAGAACACACCTTACTACA 352
Db 336 TGTAGATCTTACAGTTTACAGTTTGTGTGCTACCTGCACACACATGTACTATA 287
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RESULT 12

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US-10-147-467-1
; Sequence 1, Application US/10147467
; Publication No. US20030027295A1
; GENERAL INFORMATION:
; APPLICANT: TAKESHI, Ishii
; APPLICANT: SATOSHI, Mitsuda
; TITLE OF INVENTION: ESTERASE GENE AND ITS USE
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: FILE REFERENCE: 20-44336P
: CURRENT APPLICATION NUMBER: US/10/147,467
: CURRENT FILING DATE: 2002-05-17
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 1089
: TYPE: DNA
: ORGANISM: Burkholderia cepacia
: US-10-147-467-1

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Query Match	5.2%	Score 33.2	DB 9	Length 1089
Best Local Similarity	57.8%	Pred. No. 5.2		
Matches	59	Conservative	0	Mismatches 43
				Indels 0
				Gaps 0

[illegible]

RESULT 13
 US-09-939-964-1
 Sequence 1, Application US/09939964
 Publication No. US20030054522A1
 GENERAL INFORMATION:
 APPLICANT: Rosenthal, Andre
 APPLICANT: Freiberg, Christoph
 APPLICANT: Perret, Xavier Philippe
 APPLICANT: Broughton, William John
 TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 symbiotic
 TITLE OF INVENTION: Plasmid
 FILE REFERENCE: CARP0068
 CURRENT APPLICATION NUMBER: US/09/939,964
 CURRENT FILING DATE: 2001-08-27
 PRIOR APPLICATION NUMBER: 09/214,808
 PRIOR FILING DATE: 1999-06-22
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 1
 LENGTH: 536165
 TYPE: DNA
 ORGANISM: Rhizobium
 US-09-939-964-1

Query Match	5.1%	Score 32.8;	DB 9;	Length 536165;
Best Local Similarity	48.9%	Pred. No. 2.2e+02;		
Matches 88; Conservative	0;	Mismatches 92;	Indels 0;	Gaps 0;

QY 55 GTCAACATCGCTGTTGGGATCCACCCCTGACCAAAACCCCTGCAACCAATCCAGTTGTT 114

Db 223217 GTCCATGTTGCAACGATGCGGAACCTGGAAGAAATTTGGTCTATCCGACCAAGCTCTACGAC 223276

QY 115 ATGGTTACGGTATCCGGAGAGAGCTTCTACAACTTTCGGGAATTAAGACTCTATCCGTA 174

Db 223277 ATCTTAAGAGATGCTCGAAGAAGATATTAAGATCTTAAGAGGACGCGAAGCGAGAGCGCTGA 223356

QY 175 TCTCAGGCGCTGTCACGGGCGACGCTGATGCGGTGATTTTGGGCAACAGACGGGACG 234

Db 223337 AACGCTCTTCTGTGACCAAGGCGATCTTTGAGGCGCATGTTTTTGGACGCAACTCGGGATG 223366

RESULT 14
US-09-731-872-18
Sequence 18, Application US/09731872
Patent No. US20020102604A1
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean Baptiste
Bouqueleref, Lydie
APPLICANT: Jobert, Severin

```

? TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
? FILE REFERENCE: 78 US3 REG
? CURRENT APPLICATION NUMBER: US/09/731,872
? CURRENT FILING DATE: 2000-12-07
? PRIOR APPLICATION NUMBER: US 60/169,629
? PRIOR FILING DATE: 1999-12-08
? PRIOR APPLICATION NUMBER: US 60/187,470
? PRIOR FILING DATE: 2000-03-06
? NUMBER OF SEQ ID NOS: 482
? SOFTWARE: Patent.pm
? SEQ ID NO 18
? LENGTH: 1884
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 94..1275
? NAME/KEY: sig_peptide
? LOCATION: 94..210
? OTHER INFORMATION: Von Hejne matrix
? OTHER INFORMATION: score 4.55778392992629
? OTHER INFORMATION: seq LVLVKKRLLAIVSVS/CI
? US-09-731-872-18

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Query Match	5.1%	Score 32.6	DB 10	Length 1884
Best Local Similarity	55.9%	Pred. No. 11		
Matches 62	Conservative 0	Mismatches 45	Indels 0	Gaps 0

Oy

173 TATCTCAGGCGTGTCACGGGCAAGCTATAGCGGTGATTTTTGGACAACACAGA 232
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db

233 TATTTCCAGATGCCGTTATGGAACAAGATATCATAGATGATCTTGTGTAATAACTGA 292

Oy

233 CGAATTATACATGC GCCGCGTATATCACAGTTTGTGC AAAGTTTTAG 283
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db

293 GAGTAGATAAAAATTGCCCCAGGATCTACACAGTTAGTAATGGATTCTAG 343
||||| |||||| |

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RESULT 15
US-09-974-300-1896
Sequence 1896, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085,500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/660,558
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1896
LENGTH: 432
TYPE: DNA
ORGANISM: Bacillus licheniformis
US-09-974-300-1896

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Query Match	5.0%;	Score 32.2;	DB 10;	Length 432;
Best Local Similarity	49.1%;	Pred. No. 6.4;		
Matches	85;	Conservative	0;	Mismatches
			88;	Indels
				Gaps
				0;

QY	4	AAATTTGTAAAAAGAAAGATCATGTGCCTGTACACATTTTGGGCGTCAGACACATCG	63
Db	10	AAACTTCTAGAAATTAATGATGACGATTATTTTGGCAATTTGCTGTGGGAAACCGCTCGG	69
QY	64	CTGTTTGCAGTCAGCCGTCAGCAAAAGCCGCTGAAACACATCAGTTGTTATGTTTCAAC	123
Db	70	TTCTTTTCTCATCAAGGGAAGCGCAAGGAAAGATATCAAAACGACGAACCTTGATGATGAT	129

Mon May 19 10:47:08 2003

us-09-905-666a-1.rnpb

Page 7

OY 124 GGTATCGGAGGACCTCATACAATTTCGGGAATTAAAGCTACTTCGTATC 176
 | | | | | | | | | | | | | |
 Db 130 GAAGTGTGCAATCTTACATTGAAGTGCCGAAAATCACGACAACTTGAAATC 182

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Job time : 405 secs

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GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 18, 2003, 05:34:24 ; Search time 1077 Seconds
(without alignments)
9609.021 Million cell updates/sec

Title: US-09-905-666a-1
Perfect score: 639
Sequence: 1 atgaattgttaaaagaag.....ggggccaaatacgaattaa 639

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	42.2	6.6	1101	17	CNS00L78	AL068157 Drosophila
2	39	6.1	710	13	B1678753	B1678753 SMS601 SM
3	37.8	5.9	628	17	AL760893	AL760893 Arabidops
4	37	5.8	354	13	BG940033	BG940033 ax03b04.f
5	37	5.8	646	17	AQ989712	AQ989712 RfC00339
6	37	5.8	704	14	BQ775177	BQ775177 UI-H-PH0-

Result No.	Score	Match	Length	DB	ID	Description
7	36.8	5.8	402	14	BQ253545	BQ253545 san62e10.
8	36.8	5.8	422	10	BE555700	BE555700 sp29207.y
9	36.8	5.8	444	12	BG043888	BG043888 saa34d09.
10	36.8	5.8	495	14	BQ741211	BQ741211 saq15f10.
11	36.8	5.8	508	14	BQ079412	BQ079412 san13d01.
12	36.8	5.8	528	14	BM954819	BM954819 sam73c05.
13	36.8	5.8	539	17	BM954950	BM954950 sam75c01.
14	36.2	5.7	661	17	AQ991444	AQ991444 RfC02380
15	36.2	5.7	676	14	BQ458251	BQ458251 kos8b05.y
16	36	5.6	455	9	AT457833	AT457833 tk08f09.x
17	36	5.6	629	17	AT356293	AT356293 IM0097N16
18	36	5.6	698	17	AZ356093	AZ356093 IM0097K01
19	35.4	5.5	386	10	AW544638	AW544638 C0184B02-
20	35.4	5.5	691	13	B1969075	B1969075 GMS30007A
21	35.2	5.5	707	17	BH607139	BH607139 BOCVPE5TF
22	35.2	5.5	897	17	CNS005NL	CNS005NL Drosophila
23	35	5.5	808	17	CNS02659	CNS02659 Telradon
24	35	5.5	1101	17	CNS0183L	CNS0183L Drosophila
25	34.8	5.4	664	17	A2522069	A2522069 201PBc08
26	34.8	5.4	945	17	CNS0130R	CNS0130R AV536563
27	34.6	5.4	408	10	BM965989	BM965989 AV536563
28	34.6	5.4	426	14	BM965977	BM965977 ko20c12.y
29	34.6	5.4	548	14	BM965977	BM965977 ko20b07.y
30	34.6	5.4	567	14	BQ089146	BQ089146 ko22c11.y
31	34.6	5.4	620	14	BQ458269	BQ458269 ko58d06.y
32	34.4	5.4	631	17	A2939720	A2939720 2M0198N18
33	34.4	5.4	827	17	BH671466	BH671466 BOMPS88TR
34	34.4	5.4	947	14	BQ719062	BQ719062 AGENCOURT
35	34.4	5.4	1101	17	CNS016QS	CNS016QS Drosophila
36	34.4	5.4	1101	17	CNS0181N	CNS0181N Drosophila
37	34.2	5.4	261	12	BG319118	BG319118 NXPV_023-
38	34.2	5.4	344	14	BM815886	BM815886 EST953980
39	34.2	5.4	422	10	AV788662	AV788662 AV788662
40	34.2	5.4	1101	17	CNS012UB	CNS012UB Drosophila
41	34	5.3	900	13	BM468757	BM468757 AGENCOURT
42	34	5.3	938	17	CNS006TJ	CNS006TJ Drosophila
43	34	5.3	1304	10	BE531285	BE531285 601278207
44	33.8	5.3	437	10	BE54807	BE54807 sp81b12.y
45	33.8	5.3	438	12	BG045372	BG045372 sv42b04.y

ALIGNMENTS

RESULT 1
LOCUS CNS00L78
DEFINITION Drosophila melanogaster genome survey sequence TEn3 end of BAC: BACR24B18 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL068157
VERSION AL068157.1 GI:4958085
SOURCE Drosophila melanogaster.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see: [http://www.fruitfly.org/TheBDGP/Drosophila melanogaster BAC library](http://www.fruitfly.org/TheBDGP/Drosophila%20melanogaster%20BAC%20library) was prepared by Kazutoyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial

ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

Source

1...1101

/organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone="BACR24B18"

/clone_1lb="RPCI-98"

/note="end : TET3"

BASE COUNT 294 a 212 c 182 g 307 t 106 others

ORIGIN

Query Match 6.8%; Score 42.2; DB 17; Length 1101;

Best Local Similarity 33.2%; Pred. No. 0.13;

Matches 76; Conservative 50; Mismatches 103; Indels 0; Gaps 0;

OY 3 GAAATTTGTAAGAAGATCATGTCATGTAACATTTTGGTGTGTCAGTCACATC 62

DB 799 GAATTAATTTKAAAACACATGCAAGCATTTGTATATATTTTTRKTTT 858

OY 63 GCCTTTGGCATGACGCGGTAGCAAAAGCCGTCGACACATCCAGTTTATGTTCA 122

DB 859 TTTATCCMCGAAAAAAMWGTGAMAAAMWTCYACATTTTKVTRSCWAW 918

OY 123 CGATATCGAGAGAGCTTCATCAATTTTGGCGAATTAAGAGTATCTGATCTCAGG 182

DB 919 TKGWTWCCCTARPTTSATTAATTTCTKRATATGSKCAATRWISGAAWTTCSKTG 978

OY 183 CTGCTACGCGGCAAGCTGTATGCGGTTGATTTTGGACACAGCAGG 231

DB 979 RAGGGAAGVSCCTTTKRRARVGGKCCWTKRRGGBCGTMMVAGR 1027

RESULT 2

LOCUS

DEFINITION

B1678753 710 bp mRNA linear EST 17-SEP-2001

SMS601 SMS (Sapwood of black locust - Summer) Robinia pseudoacacia

ACCESSION B1678753

VERSION B1678753.1 GI:15631660

KEYWORDS EST

SOURCE Robinia pseudoacacia

ORGANISM Robinia pseudoacacia

REFERENCE 1 (bases 1 to 710)

AUTHORS Han, K.-H., Yang, J., Park, S., Paule, C.R., Kapur, V., Retzel, E.F.,

Kamdem, D.P. and Keathley, D.E.

ANALYSIS Analysis of gene expression patterns in trunk wood of a mature

black locust (Robinia pseudoacacia)

COMMENT Unpublished (2002)

CONTACT Contact: Kyung-Hwan Han

DEPARTMENT Department of Forestry

INSTITUTION Michigan State University

ADDRESS 126 Natural Resources, East Lansing, MI 48824-1222, USA

TEL 517 353 4751

FAX 517 432 1143

EMAIL Email: hanky@msu.edu

LOCATION/Qualifiers

1. 710

/organism="Robinia pseudoacacia"

/db_xref="taxon:35938"

/clone_1lb="SMS (Sapwood of black locust - Summer)"

/tissue_type="sapwood"

/dev_stage="mature tree"

/note="Vector: lambda Triplex; Site 1: Sfi IA; Site 2: Sfi

IB; The cDNA library was made from the sapwood of a mature

black locust tree collected in Michigan in late July."

BASE COUNT 252 a 124 c 101 g 228 t 5 others

ORIGIN

Query Match 6.1%; Score 39; DB 13; Length 710;

Best Local Similarity 61.2%; Pred. No. 1;

Matches 63; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

OY 418 ACGACAGCAAGCGCTCCGGAGACAGATCCAAATCAAGATTTTATACATCCATT 477

DB 264 ACTAACAGCTCATGATTCAGAAATGCAATGCAATGCAATGCAATGCAATGCAAT 323

OY 478 TACGACAGTCCGATGATGATGATGATGATGATGATGATGATGATGATGAT 520

DB 324 TAAATAATGAAATTCAAATGACATTAATTAATTAATTAATTAATTAAT 366

RESULT 3

LOCUS

DEFINITION

AL760893/c 628 bp DNA linear GSS 19-JUN-2002

Arabidopsis thaliana T-DNA flanking sequence GK-203f11-014507,

genomic survey sequence.

ACCESSION AL760893

VERSION AL760893.1 GI:21501099

KEYWORDS GSS.

SOURCE thale cress.

ORGANISM Arabidopsis thaliana

REFERENCE 1

AUTHORS Strizhov, N., Li, Y., Rosso, M., Viehovec, P., Dekker, K., Saedler, H.

and Weisshaar, B.

TITLE A pipeline for automated high-throughput generation of FSTs

(flanking sequence tags) from Arabidopsis thaliana T-DNA

transformed lines

UNPUBLISHED

REFERENCE 2

AUTHORS Rosso, M., Strizhov, N., Li, Y., Reiss, B., Dekker, K. and Weisshaar, B.

TITLE A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)

for flanking sequence tag based reverse genetics

UNPUBLISHED

REFERENCE 3 (bases 1 to 628).

AUTHORS Li, Y., Strizhov, N., Rosso, M. and Weisshaar, B.

TITLE Direct Submission

COMMENT Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer

Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence is recovered from the left border of the T-DNA. It

indicates an insertion close to or within gene At2g19740. The

sequences are generated at the MPI for Plant Breeding Research in

the context of the GABI-Kat project. GABI-Kat is part of the German

Plant Genomics program designated 'GABI'. Information on line

availability can be found at:

<http://www.mpi-zkoeln.mpg.de/GABI-Kat/>.

LOCATION/Qualifiers

1. 628

/organism="Arabidopsis thaliana"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="GK-203f11-014507"

/clone_1lb="Arabidopsis thaliana T-DNA insertion lines"

/note="PCR was performed on DNA from Arabidopsis thaliana

plants (T1) which were transformed with the T-DNA from

vector pAC161. The lines contain one or more T-DNA

insertions. The DNA fragment(s) resulting from the PCR

were directly sequenced to determine the genomic sequence

flanking the insertion. Sequences displaying significant

similarity to the A. thaliana nuclear genome sequence were

processed for submission. T-DNA derived sequences were

removed"

BASE COUNT 214 a 100 c 102 g 212 t

ORIGIN


```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ax03b04"
/clone_1_id="Proliferating Human Erythroid Cells (LCB:ax
library)"
/sex="unknown"
/tissue_type="blood"
/cell_type="Erythroid Cells"
/cell_line="Primary Culture of Peripheral Blood
Mononuclear Cells"
/dev_stage="Progenitor; EPO responsive CD71++++"
/lab_host="SOLR"
/note="Organ: blood; Vector: Lambda ZAP II; Site_1: EcoRI
Site_2: EcoRI; 65,000 proliferating erythroid cells from
the buffy coat of a blood donation were obtained by flow
cytometric separation after a 5-day culture period in the
presence of erythropoietin. Total RNA was purified from
the sorted cell population using RNeasy reagent. RNA (0.3
ug) was converted into double stranded cDNA using
Clontech's CapFinder cDNA Library Construction Kit
(Clontech) according to the manufacturer's protocol and
cloned into EcoRI digested lambda zap II vector
(Stratagene). The phage library was amplified once prior
to in vivo excision in SOLR cells. Individual colonies
were grown, and the cDNA inserts were sequenced in high

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Query Match	5.88; Score 37; DB 17; Length 646;
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[illegible]

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Query Match Similarity      5.8%; Score 37; DB 14; Length 704;
Best Local Similarity      50.3%; Pred. No. 4;
Matches      91; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

OY 450 AATCAAAAATTTTATACACATTCATTTAGACGAGTCCGATATGATTCATGATTA 509
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 278 AATTAATAGATTTTATATATATGTGTATATATATATATATATATTAAGCATTAACGT 337
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 510 CTTATCAAAATTTAGACGGTGTCTAAAAAGCTCAATTCATGTGGCGTTCATTGGTT 569
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 338 TTCAACCAATATATACAAAGTGCAMACATACAAAAATCCCACTATCTGTATCAGGAGCC 397
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 570 ATTGATGAACAGCCCAAGTCACACAGCCTGATTTAAAGAGACTGAACGGCGGCCCAAA 629
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 398 ATTTACGCTCCCGAACAACAGAGCTTATCAGCGTTCCTGCACTGGGGGGACACAG 457
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 630 T 630
      |
DB 458 T 458

RESULT 7
BQ253545/c 402 bp mRNA linear EST 03-MAY-2002
LOCUS
DEFINITION
Gm-c1052-4435 5', mRNA sequence.
ACCESSION
BQ253545
VERSION
BQ253545.1 GI:20449421
KEYWORDS
EST.
SOURCE
soybean.
ORGANISM
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1..(bases 1 to 402)
Shoemaker,R., Keim,P., Vodkin,L., Erpelidng,J., Coryell,V., Khanna
,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wylie,T., Underwood,K., Stepien,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurr
,R., Ritters,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Hunttsville, AL 35801 For further information
call: (800)-533-4363 or contact: ccl@resgen.com web site:
www.resgen.com
Seq primer: -40RP from Gldco
High quality sequence stop: 370.
Location/Qualifiers
1..402
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1052-4435"
/clone_lib="Gm-c1052"
/tissue_type="whole seedlings of greenhouse grown plants"
/dev_stage="1 week old"
/db_host="DH10B"
/note="Vector: Bluescript II SK+, Site_1: EcoRI; Site_2:
XhoI; The Harosoy NIL was constructed and seed was
provided by Dr. J. Specht, University of Nebraska
(Shoemaker and Specht, 1995). The cDNA library was
constructed from mRNA isolated from whole seedlings of 1
week old greenhouse grown plants. Complementary DNA was

```


fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed in the laboratory of Dr. Randy Shoemaker at Iowa State University."

BASE COUNT 133 a 116 c 92 g 103 t
ORIGIN

Query Match 5.8% Score 36.8; DB 12; Length 444;

Best Local Similarity 69.4% Pred. No. 3.9;

Matches 50; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 2 TGAATTGTGTAAGAAGATCATTCACATTTGGTGTCTGCTACATCAT 61

Db 160 TGAATTGGGAAGAAGAGGATTTTGTGTGGGATCTGTATTATGTCGCACAT 101

QY 62 CGCTGTTGGCA 73

Db 100 CGCAGTTGGGGA 89

RESULT 10

BO741211/c

LOCUS BO741211 495 bp mRNA linear EST 17-JUN-2002

DEFINITION seq15f10.y1 Gm-c1045 glycine max cDNA clone SOYBEAN CLONE ID: 5';

ACCESSION BO741211

VERSION BO741211.1 GI:21887998

KEYWORDS EST

SOURCE soybean.

ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

1 (bases 1 to 495)

REFERENCE

AUTHORS

Shoemaker, R., Keim, P., Vodkin, L., Erpelidg, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Public Soybean EST Project

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: Resgen, Invitrogen Corp. 2130

South Memorial Parkway Huntsville, AL 35801 For further information

call: (800)-533-4363 or contact: ccu@resgen.com web site:

www.resgen.com

FEATURES

source

1. 495

/db_xref="taxon:3847"

/clone="SOYBEAN CLONE ID: 5"

/issue_type="Gm-c1045"

/lab host="DH10B"

/note="Vector: pBluescript II SK⁺, Site 1: EcoRI, Site 2:

XhoI; This cDNA library was constructed from mRNA isolated

from etiolated hypocotyl tissue of 9-10 day old seedlings

of the cultivar Williams 82. Complementary DNA was

synthesized from mRNA using a primer consisting of a

poly(GT) primer with a XhoI restriction site; EcoRI

adapters were ligated to the blunt-ended cDNA fragments

followed by digestion with EcoRI and XhoI. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker."

BASE COUNT 141 a 138 c 101 g 115 t
ORIGIN

Query Match 5.8% Score 36.8; DB 14; Length 495;

Best Local Similarity 69.4% Pred. No. 4.1;

Matches 50; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 2 TGAATTGTGTAAGAAGATCATTCACATTTGGTGTCTGCTACATCAT 61

Db 193 TGAATTGGGAAGAAGAGGATTTTGTGTGGGATCTGTATTATGTCGCACAT 134

QY 62 CGCTGTTGGCA 73

Db 133 CGCAGTTGGGGA 122

RESULT 11

BO079412/c

LOCUS BO079412 503 bp mRNA linear EST 04-APR-2002

DEFINITION san13d01.y1 Gm-c1084 glycine max cDNA clone SOYBEAN CLONE ID:

Gm-c1084-3626 5', mRNA sequence.

ACCESSION BO079412

VERSION BO079412.1 GI:19934382

KEYWORDS EST

SOURCE soybean.

ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

1 (bases 1 to 503)

REFERENCE

AUTHORS

Shoemaker, R., Keim, P., Vodkin, L., Erpelidg, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Public Soybean EST Project

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project

Public Soybean EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: Resgen, Invitrogen Corp. 2130

South Memorial Parkway Huntsville, AL 35801 For further information

call: (800)-533-4363 or contact: ccu@resgen.com web site:

www.resgen.com

FEATURES

source

1. 503

/db_xref="taxon:3847"

/clone="SOYBEAN CLONE ID: Gm-c1084-3626"

/issue_type="Gm-c1084"

/lab host="DH10B"

/note="Vector: pBluescript II SK⁺, Site 1: EcoRI, Site 2:

XhoI; The cDNA library was constructed by M. Bhattacharya

from mRNA isolated from etiolated hypocotyls from the

cultivar Williams 82. Tissue was inoculated with

Phytophthora soyae race 1 and tissues were harvested 2 and

4 hours following infection. The library is the pool of

these two time points. Complementary DNA was synthesized

seedlings or the cultivar Williams. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the palunscript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy

	Shoemaker."			
BASE COUNT	146 a	143 c	120 g	119 t

Overall Match 5 08 : 55000 36 0 : DB 14 : Tomath 538 :

Best Local Similarity	69.48;	Pred. No. 4.2;

2 TGAATTTGTAAGAGAGATCATTCACCTTGTAACAATTTGGTGTGTACAT 61

[illegible]

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RESOL 13
BM954950/c

LOCUS	BM954950	539 bp.	mRNA	Linear	EST	14-MAR-2002
DEFINITION	sam75c01.v1 Gm-cl069 Glycine max cDNA clone SOYBEAN CLONE ID:					

Gm-C1069-5113 5', mRNA sequence:
BM054950

VERSION BM954950.1 GI:19453540

KEYWORDS	ESI.
SOURCE	soybean.

ORGANISM	Glycine max
Eukaryota: Viridiplanta	

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae: eurosids I: Fabales: Fabaceae: Papilionoideae: Phaseoleae: Psidium

Glycine.

AUTHORS Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna

A., Bolla, B., Marfa, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers

Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurck
P. Bitter E. Kohn S. Shin T. Jackson Y. Cardenas M. McCann

, R., Waterston, R. and Wilson, R.

FILE
FABRIC 30year ESI Project
JOURNAL
Unpublished (1999)

COMMENT:
Contact: Shoemaker R/Public soybean EST Project
Public Soybean EST Project

Washington University School of Medicine
444 Forest Park Parkway Box 8501 St. Louis MO 63108 USA

Tel: 314 286 1800

FAX: 014 200 1010
 Email: est@watson.wustl.edu

This clone is available through: Resgen, Invitrogen corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information

call: (800)-533-4363 or contact: ccu@resgen.com web site:
www.resgen.com

Seq primer: -40RP from Gibco

high quality sequence stop: 422.
Location/Qualifiers

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source
1. .539
/organism="Glycine max"
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/db_xref="taxon:3847"
/clone="SOVBEAN CDONE TD: Cn-01060-5113"

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/clone_lib="Gm-cl069"
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7 tissue-type - degenerating cotyledons, 5 to 60 day old
etiolated seedling"

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/lab_host="DH10B"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:

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XhoI; The cDNA library was constructed from mRNA isolated

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